

1  
GATCATTAAATAAATCAAGGTTAGTTAGCTTGAAAGATATAAATATATTCCAAAATTCCA  
61  
AAAAGTAATTGGCATAGTGACAAAACTATTGCTCCCCTGCTTTAGAAATAATTTATTTT  
121  
TAATTTAATATTTAAAAGTAACTGAAGAATCTAGTTATATTTAAAAAGTAAAGGTTGCAT  
181  
TTTAACTAAATTATGTTAACTACTGTTATGCGATGAGTCGATATGTGGTTTTACCACTA  
241  
TTGCGCAGGGAGATTATAAACGCAGGAGCGGATCTTGATAAGTTGTGTGAACCTTCTTGT  
301  
CACACTTGAAAAGGTGCCCTTAGCTTACTACTACTTGTAAATTTCTTACAAATTGTGGTAA  
361  
GTAGCTGAAAAGCAAAAAAGAAAGAACCAAGTTTGGTTCTTTCTTTTTTGCATAAATAAGT  
421  
CACAAATTCCTTCTTAAAATTATGTCTTTACTTAACTTTAATTGAATATGCTACCATCAC  
481  
ATTCTTTGTAAATTTTTTAAATAATCTAGTTTCTGATGGTTTAGATGAAGTATTAAAAAT  
541  
ATACTATTACCTCATTGTAAATCTTAATGTTAGTATGACTATCTATCATGCTTTATAATA  
601  
TTAAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTAATTTTAAACATACA  
661  
AATTAATAATAAATTGCAACTAAATAATAAATTATCTTGACATAACTTATAAAATGTTTT  
721  
AATATATAATCTAAATAAAAAGTAATAATAAAATGACTTTTAAAATTTAAAAAAAGTAAGG  
781 RBS  
AGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAATCAGGAAAGCTTTGGCT  
841 M F N K I G F R T W K S G K L W L  
TTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTCCTGTATCTGCTATGGA  
Y M G V L G S T I I L G S S P V S A M D  
901  
TAGTGTTGGAAATCAAAGTCAGGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAA  
S V G N Q S Q G N V L E R R Q R D A E N  
961 Repeat 2 (SEQ ID 22)  
CAGAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACGCGATGTTGAGAATAAGAGCCAAGG  
R S Q G N V L E R R Q R D V E N K S Q G  
1021 Repeat 4 (SEQ ID 24)  
CAATGTTTTAGAGCGTCGTCAACGTGATGCGGAAAACAAGAGCCAAGGCAATGTTTTAGA  
N V L E R R Q R D A E N K S Q G N V L E  
1081 Repeat 5 (SEQ ID 25)  
GCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACG  
R R Q R D A E N R S Q G N V L E R R Q R  
1141 Repeat 6 (SEQ ID 26)  
TGATGCAGAAAACAGAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACGCGATGCAGAAAA

Fig. 1-1

Best Available Copy

D A E N R S Q G N V L E R R Q R D A E N  
1201 Repeat 7 (SEQ ID 27) Repeat 8 (SEQ ID 28)  
CAGAAGCCAAAGGTAATGTTCTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAAGG  
R S Q G N V L E R R Q R D A E N R S Q G  
1261 Repeat 9 (SEQ ID 29)  
TAATGTTCTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGTAATGTTCTAGA  
N V L E R R Q R D A E N R S Q G N V L E  
1321 Repeat 10 (SEQ ID 30)  
GCGTCGTCAACGCGATGTTGAGAATAAGAGCCAAGGCAATGTTTATAGAGCGTCGTCAACG  
R R Q R D V E N K S Q G N V L E R R Q R  
1381 Repeat 11 (SEQ ID 31)  
TGATGCGGAAAACAAGAGCCAAGGCAATGTTTATAGAGCGTCGTCAACGTGATGCAGAAA  
D A E N K S Q G N V L E R R Q R D A E N  
1441 Repeat 12 (SEQ ID 32) Repeat 13 (SEQ ID 33)  
CAGAAGCCAAAGGCAATGTTTATAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAAGG  
R S Q G N V L E R R Q R D A E N R S Q G  
1501 Repeat 14 (SEQ ID 34)  
CAATGTTCTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGCAATGTTCTAGA  
N V L E R R Q R D A E N R S Q G N V L E  
1561 Repeat 15 (SEQ ID 35)  
GCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACG  
R R Q R D A E N R S Q G N V L E R R Q R  
1621 Repeat 16 (SEQ ID 36)  
CGATGCAGAAAACAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGTGATGCAGAAA  
D A E N R S Q G N V L E R R Q R D A E N  
1681 Repeat 17 (SEQ ID 37) Repeat 18 (SEQ ID 38)  
CAGAAGCCAAAGGCAATGTTTATAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAAGG  
R S Q G N V L E R R Q R D A E N R S Q G  
1741 Repeat 19 (SEQ ID 39)  
CAATGTTTATAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGCAATGTTTATAGA  
N V L E R R Q R D A E N R S Q G N V L E  
1801  
GCGTCGTCAACGTGATGCGGAAAACAAGAGCCAAGTAGGTCAACTTATAGGGAAAAATCC  
R R Q R D A E N K S Q V G Q L I G K N P  
1861  
ACTTCTTTCAAAGTCAATTATATCTAGAGAAAATAATCACTCGAGTCAAGGTGACTCTAA  
L L S K S I I S R E N N H S S Q G D S N  
1921  
CAAACAGTCATTCTCTAAAAAAGTATCTCAGGTTACTAATGTAGCTAATAGACCGATGTT  
K Q S F S K K V S Q V T N V A N R P M L  
1981  
AACTAATAATTCTAGAACAAATTTTCAGTGATAAATAAATTACCTAAAACAGGTGATGATCA  
T N N S R T I S V I N K L P K T G D D Q  
2041

Fig. 1-2

10/531 659

AAATGTCATTTTTAAACTTGTAGGTTTGGTTTAATTTTGTTAACAAGTCGCTGCGGTTT  
N V I F K L V G F G L I L L T S R C G L  
2101  
GAGACGCAATGAAAATTAAGTATAATCAATCATTTAGTAACTATATATAATGATATATGC  
R R N E N \*  
2161  
AATCAATAAAAAGGAATCGGATACGAGATTCCTTTTTATAATTAGGTTGGTTAGGGTGAC  
2221  
TTTTTTCATTTGGCTATTCTTGAAAGTTTATAAAAATGTAGTTATAATAGTCACATTAAA  
2281  
ATGTTTTGAAAATATTGATGAACAACATCAACAAATAGAGGTCATTATATGGGATATACC  
2341  
GTTGCTATCGTAGGTGCTACAGGTGCCGTAGGAACACAAATGATTCGTCAATTAGAACAA  
2401  
TCGAATTTACCAATAGAACAAGTGAACTTTTATCATCAAGTCGCTCAGCAGGTAAAATT  
2461  
TTACATTTTAAAGATGAGGCTATACGTGTTGAAGAGACAACAAAAGAATCATTTTACGAT  
2521  
GTTGATATTGCCTTGTTTTTCAGCTGGTGGATC

Fig. 1-3

Inventor: Reinscheid et al.

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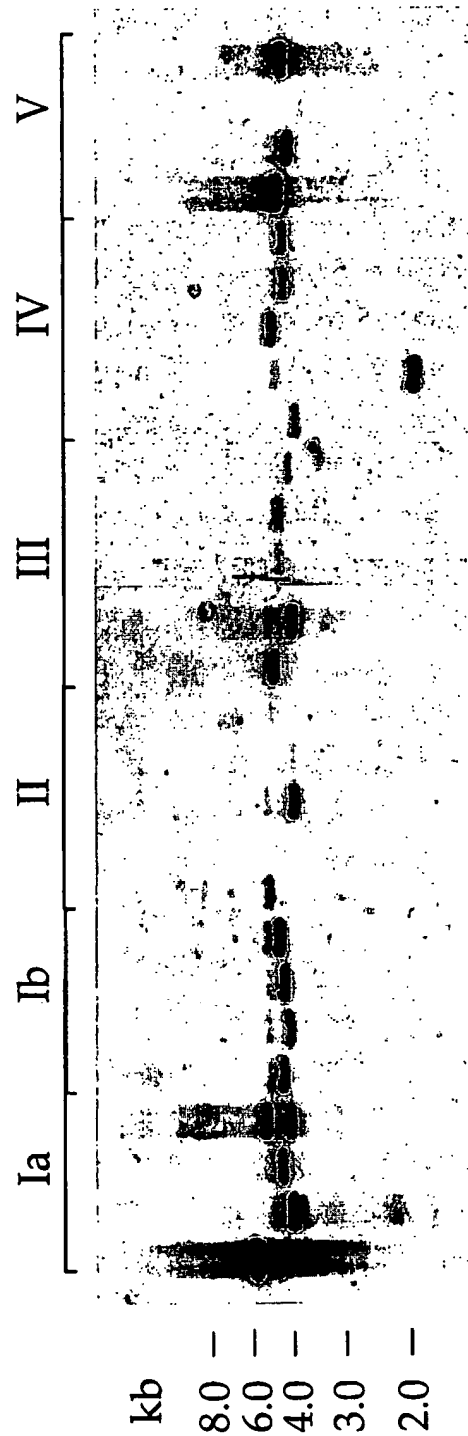


Fig. 2

1  
GCATAAATAAGTCACAATTCCTTCTTAAAATTATGTCTTTACTTAACTTTAATTGAATA  
61  
TGCTACCATCACATTCTTTGTAAAATTTTAAATAATCTAGTTTCTGATGGTTTAGATGA  
121  
AGTATTAAAAATATACTATTACCTCATTGTAAATCTTAATGTTAGTATGACTATCTATCA  
181  
TGCTTTATAATATTAAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTAAT  
241  
TTTAAACATACAAATTAATAATAAATTGCAACTAAATAATAAATTATCTTGACATAACTT  
301  
ATAAAATGTTTTAATATATAATCTAAATAAAAGTAATAATAAAATGACTTTTAAAATTTA  
361  
AAAAAAGTAAGGAGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAATCAGG  
421 RBS M F N K I G F R T W K S G  
AAAGCTTTGGCTTTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTTCTGT  
K L W L Y M G V L G S T I I L G S S S V  
481 Repeat 1 (SEQ ID 40)  
ATCTGCTATGGATAGTGTGGAAATCAAAGTCAGGGCAATGTTTTAGAGCGTCGTCAACG  
S A M D S V G N Q S Q G N V L E R R Q R  
541 Repeat 2 (SEQ ID 41)  
CGATGCAGAAAACAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAA  
D A E N R S Q G N V L E R R Q R D A E N  
601 Repeat 3 (SEQ ID 42) Repeat 4 (SEQ ID 43)  
CAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGG  
R S Q G N V L E R R Q R D A E N R S Q G  
661 Repeat 5 (SEQ ID 44)  
TAATGTTCTAGAGCGTCGTCAACGCGATGTTGAAAATAAAAGCCAAGGCAATGTTTTAGA  
N V L E R R Q R D V E N K S Q G N V L E  
721 Repeat 6 (SEQ ID 45)  
GCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACG  
R R Q R D A E N R S Q G N V L E R R Q R  
781 Repeat 7 (SEQ ID 46)  
CGATGTTGAAAATAAAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAA  
D V E N K S Q G N V L E R R Q R D A E N  
841 Repeat 8 (SEQ ID 47) Repeat 9 (SEQ ID 48)  
CAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGG  
R S Q G N V L E R R Q R D A E N R S Q G  
901 Repeat 10 (SEQ ID 49)  
CAATGTTTTAGAGCGTCGTCAACGCGATGCAGAAAACAGAAGCCAAGGCAATGTTCTAGA  
N V L E R R Q R D A E N R S Q G N V L E

Fig. 3-1

961 Repeat 11 (SEQ ID 50) →  
GCGTCGTCAACGTGATGCTGAAAAACAAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACG  
R R Q R D A E N K S Q G N V L E R R Q R  
1021 Repeat 12 (SEQ ID 51) →  
TGATGCAGAAAACAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCTGAAAA  
D A E N R S Q G N V L E R R Q R D A E N  
1081 Repeat 13 (SEQ ID 52) Repeat 14 (SEQ ID 53) →  
CAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGCGATGCAGAAAACAGAAGCCAAGG  
R S Q G N V L E R R Q R D A E N R S Q G  
1141 Repeat 15 (SEQ ID 54) →  
TAATGTTCTAGAGCGTCGTCAACGTGATGCGGAAAACAAGAGCCAAGGCAATGTTTTAGA  
N V L E R R Q R D A E N K S Q G N V L E  
1201 Repeat 16 (SEQ ID 55) →  
GCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGCAATGTTTTAGAGCGTCGTCAACG  
R R Q R D A E N R S Q G N V L E R R Q R  
1261 Repeat 17 (SEQ ID 56) →  
CGATGTTGAGAATAAGAGCCAAGGCAATGTTTTAGAGCGTCGTCAACGTGATGCGGAAAA  
D V E N K S Q G N V L E R R Q R D A E N  
1321  
CAAGAGCCAAGTAGGTCAACTTATAGGGAAAAATCCACTTCTTTCAAAGTCAATTATATC  
K S Q V G Q L I G K N P L L S K S I I S  
1381  
TAGAGAAAATAATCACTCTAGTCAAGGTGACTCTAACAAACAGTCATTCTCTAAAAAAGT  
R E N N H S S Q G D S N K Q S F S K K V  
1441  
ATCTCAGGTTACTAATGTAGCTAATAGACCGATGTTAATAATAATTCTAGAACAATTTTC  
S Q V T N V A N R P M L T N N S R T I S  
1501  
AGTGATAAATAAATTACCTAAAACAGGTGATGATCAAAATGTCATTTTTAACTTGTAGG  
V I N K L P K T G D D Q N V I F K L V G  
1561  
TTTTGGTTTAATTTTGTTAACAAGTCGCTGCGGTTTGAGACGCAATGAAAATTAAGTATA  
F G L I L L T S R C G L R R N E N \*  
1621  
ATCAATCATTTAGTAACTATATATAATGATATATGCAATCAATAAAAAGGAATCGGATAC  
←  
GAGATTCCTTTTTATAATTAGGTTGGTTAGGGTGACTTTTTTCATTTGGCTATTCTTGAA  
1741 1761 1781  
AGTTTATAAAAATGTAGTATAATAGTCACATTAAAATGTTTTGAAAATATTGATGAACAA  
1801  
CATCAACAAATAGAGGTCAT

Fig. 3-2

1  
GCATAAATAAGTCACAATTTCTTCTAAAAATTATGTCTTTACTTAACTTTAATTGAATA  
61  
TGCTACCATCACATTCTTTGTAAAATTTTTAAATAATCTAGTTTCTGATGGTTTAGATGA  
121  
AGTATTAAAAATATACTATTATCTCATTGTAAATCCTAATGTTAGTATGACTATCTATCA  
181  
TGTTTTATAATATTGAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTAAT  
241  
TTTAAACATACAAATTAATAATAAATTGCAATTAAATAACAAATTACCTTGACATAAATT  
301  
ATAAAATGTTTTAATATATATAATCTAAATAAAAAATAATAATAAAATGACTTTTAAATT  
361  
TAAAAAAGTAAGGAGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAATCA  
421  
RBS M F N K I G F R T W K S  
GGAAAGCTTTGGCTTTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTCCT  
G K L W L Y M G V L G S T I I L G S S P  
481  
Repeat 1 (SEQ ID 57) →  
GTATCTGCTATGGATAGTGTGGAAATCAAAGTCAAGGTAATGTTCTAGAGCGTCGTCAA  
V S A M D S V G N Q S Q G N V L E R R Q  
541  
Repeat 2 (SEQ ID 58) →  
CGTGATGCGGATAACAAGAGCCAAGGCAATGTTCTAGAACGTCGTCAACGCGATGTAGAA  
R D A D N K S Q G N V L E R R Q R D V E  
601  
Repeat 3 (SEQ ID 59) →  
AACAGAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACGCGATGCGGATAACAAGAGCCAA  
N R S Q G N V L E R R Q R D A D N K S Q  
→ Repeat 4 (SEQ ID 60) Repeat 5 (SEQ ID 61) →  
GGCAATGTTTTAGAGCGCCGCCAACGCGATGCAGAAAACAAAAGTCAGGCAATGTTCTA  
G N V L E R R Q R D A E N K S Q G N V L  
721  
Repeat 6 (SEQ ID 62) →  
GAACGTCGTCAACGTGATGTTGAGAATAAGAGCCAAGGCAATGTTCTAGAGCGTCGCCAA  
E R R Q R D V E N K S Q G N V L E R R Q  
781  
Repeat 7 (SEQ ID 63) →  
CGTGATGCAGAAAACAAAAGTCAGGGTAATGTTCTAGAGCGTCGTCAACGCGATGCAGAT  
R D A E N K S Q G N V L E R R Q R D A D  
841  
Repeat 8 (SEQ ID 64) →  
AACAAGAGCCAAGGTAATGTTCTAGAACGTCGTCAACGCGATGTGAAAACAAAAGTCAG  
N K S Q G N V L E R R Q R D V E N K S Q  
→ Repeat 9 (SEQ ID 65) Repeat 10 (SEQ ID 66) →  
GGCAATGTTCTAGAACGTCGTCAACGTGATGTTGAGAATAAGAGCCAAGGCAATGTTCTA  
G N V L E R R Q R D V E N K S Q G N V L  
961  
Repeat 11 (SEQ ID 67) →  
GAGCGTCGCCAACGTGATGCAGAAAACAAAAGTCAGGGTAATGTTCTAGAGCGTCGTCAA  
E R R Q R D A E N K S Q G N V L E R R Q

Fig. 4-1

Inventor: Reinscheid et al.

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1021 Repeat 12 (SEQ ID 68) →  
CGCGATGCAGATAACAAGAGCCAAGGTAATGTTCTAGAACGTCGTCACGCGATGTGGAA  
R D A D N K S Q G N V L E R R Q R D V E  
1081 → Repeat 13 (SEQ ID 69)  
AACAAAAGTCAGGGCAATGTTCTAGAGCGTCGCCAACGTGATGTTGAGAACAAGAGCCAA  
N K S Q G N V L E R R Q R D V E N K S Q  
1141  
GTAGGTCAACTTATAGGGAAAAATCCACTTCTTTCAAAGTCAACTATATCTAGAGAAAAT  
V G Q L I G K N P L L S K S T I S R E N  
1201  
AATCACTCTAGTCAAGGTGACTCTAACAAACAGTCATTCTCTAAAAAGTATCTCAGGTT  
N H S S Q G D S N K Q S F S K K V S Q V  
1261  
ACTAATGTAGCTAATAGACCAATGTTAACTAATAATTCTAGAACAATTTTCAGTGATAAAT  
T N V A N R P M L T N N S R T I S V I N  
1321  
AAATTACCTAAACAGGTGATGATCAAAATGTCATTTTTAAACTTGTAGGTTTTGGTTTA  
K L P K T G D D Q N V I F K L V G F G L  
1381  
ATTTTGTTAACAAGTCGCTGCGGTTTGAGACGCAATGAAAATTAAGTATAATCAATCATT  
I L L T S R C G L R R N E N \*  
1441  
TAGTA ACTATTATAATGATATATGCAATCAATAAAAAGGAATCGGATACAAGATTCCTTT  
TTATAATTAGGTTGGTTAGGGTGACTTTTTCATTTGGCTATTCTTGAAAGTTTATAAAAA  
1561  
TG TAGTATAATAGTCACATTAAAATGTTTTGAAAATATTGATGAACAACATCAACAAATA  
1621  
GAGGTCAT

Fig. 4-2



10/531659

1  
GCATAAATAAGTCACCAATTTCCCTTCTTAAAATTATGTCCTTTACTTTAACTTTAATTGAA  
61  
TATGCTACCATCACATTCTTTGTAAAATTTTAAATAATCTAGTTTCTGATGGTTTAGAT  
121  
GAAGTATTAAAAATATACTATTACCTCATTGTAAATCTTAATGTTAGTATGACTATCTAT  
181  
CATGCTTTATAATATTAAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTA  
241  
ATTTTAAACATACAAATTAATAATAAATTGCAACTAAATAATAAATTATCTTGACATAAC  
301  
TTATAAAATGTTTTAATATATAATCTAAATAAAAGTAATAATAAAATGACTTTTAAATT  
361  
TAAAAAAGTAAGGAGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAAATCA  
421  
RBS M F N K I G F R T W K S  
GGAAAGCTTTGGCTTTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTCCT  
G K L W L Y M G V L G S T I I L G S S P  
481  
Repeat 1 (SEQ ID 70) →  
GTATCTGCTATGGATAGTGTGGAATCAAAGTCAGGGCAATGTTTTAGAGCGTCGTCAA  
V S A M D S V G N Q S Q G N V L E R R Q  
541  
Repeat 2 (SEQ ID 71) →  
CGCGATGCAGAAAACAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGCGATGCAGAA  
R D A E N R S Q G N V L E R R Q R D A E  
601  
Repeat 3 (SEQ ID 72) →  
AACAGAAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGTGATGCGGAAAACAAGAGCCAA  
N R S Q G N V L E R R Q R D A E N K S Q  
661  
GTAGGTCAACTTATAGGGAAAAATCCACTTCTTTCAAAGTCAATTATATCTAGAGAAAAT  
V G Q L I G K N P L L S K S I I S R E N  
721  
AATCACTCTAGTCAAGGTGACTCTAACAAACAGTCATTCTCTAAAAAGTATCTCAGGTT  
N H S S Q G D S N K Q S F S K K V S Q V  
781  
ACTAATGTAGCTAATAGACCGATGTAACTAATAATTCTAGAACAATTTTCAGTGATAAAT  
T N V A N R P M L T N N S R T I S V I N  
841  
AAATTACCTAAACAGGTGATGATCAAAATGTCATTTTAACTTGTAGGTTTTGGTTTA  
K L P K T G D D Q N V I F K L V G F G L  
901  
ATTTTGTTAACAAGTCGCTGCGGTTTGAGACGCAATGAAAATTAAGTATAATCAATCATT  
I L L T S R C G L R R N E N \*  
961  
TAGTAACTATATATAATGATATATGCAATCAATAAAAAGGAATCGGATACGAGATTCCTT  
TTTATAATTAGGTTGGTTAGGGTGACTTTTTTCATTTGGCTATTCTTGAAAGTTTATAAA  
1081  
AATGTAGTATAATAGTCACATTAAAATGTTTTGAAAATATTGATGAACAACATCAACAAA  
1141  
TAGAGGTCAT

Fig. 5

1

GCATAAATAAGTCACAATTTCTTCTTAAATTATGTCCTTTACTTAACTTTAATTGAATA  
61

TGCTACCATCACATTCTTTGTAAAATTTTAAATAATCTAGTTTCTGATGGTTTAGATGA  
121

AGTATTAAAAATATACTATTACCTCATTGTAAATCTTAATGTTAGTATGACTATCTATCA  
181

TGCTTTATAATATTAAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTAAT  
241

TTTAAACATACAAATTAATAATAAATTGCAACTAAATAATAAATTATCTTGACATAACTT  
301

ATAAAATGTTTTAATATATAATCTAAATAAAAGTAATAATAAAATGACTTTTAAATTTA  
361

AAAAAGTAAGGAGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAATCAGG  
421

RBS M F N K I G F R T W K S G  
AAAGCTTTGGCTTTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTCCTGT  
K L W L Y M G V L G S T I I L G S S P V

481 Repeat 1 (SEQ ID 73) →  
ATCTGCTATGGATAGTGTGGAATCAAAGCCAAGGCAATGTTCTAGAGCGTCGTCAACG

S A M D S V G N Q S Q G N V L E R R Q R  
541 Repeat 2 (SEQ ID 74) →

CGATGCAGAAAACAGAAGCCAAGGTAATGTTTTAGAACGTCGTCAACGCGATGTTGAGAA  
D A E N R S Q G N V L E R R Q R D V E N

601 Repeat 3 (SEQ ID 75) → Repeat 4 (SEQ ID 76) →  
CAAGAGCCAAGGTAATGTTTTAGAGCGTCGCCAACGTGATGCGGAAAACAAAAGTCAGGG

K S Q G N V L E R R Q R D A E N K S Q G  
661

Repeat 5 (SEQ ID 77) →  
CAATGTTTTAGAGCGTCGTCAACGTGATGCAGAAAACAGAAGCCAAGGTAATGTTCTAGA

N V L E R R Q R D A E N R S Q G N V L E  
721

Repeat 6 (SEQ ID 78) →  
GCGTCGTCAACGCGATGTTGAGAATAAGAGCCAAGGCAATGTTCTAGAGCGTCGTCAACG

R R Q R D V E N K S Q G N V L E R R Q R  
781

Repeat 7 (SEQ ID 79) →  
CGATGTTGAGAATAAGAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGCGATGTTGAGAA

D V E N K S Q G N V L E R R Q R D V E N  
841

Repeat 8 (SEQ ID 80) → Repeat 9 (SEQ ID 81) →  
TAAGAGCCAAGGTAATGTTCTAGAGCGTCGTCAACGTGATGCGGAAAACAAGAGCCAAGG

K S Q G N V L E R R Q R D A E N K S Q G  
901

Repeat 10 (SEQ ID 82) →  
CAATGTTCTAGAGCGTCGTCAACGCGATGCAGAAAACAGAAGCCAAGGTAATGTTTTAGA

N V L E R R Q R D A E N R S Q G N V L E  
961

GCGTCGCCAACATGATGTTGAGAATAAGAGTCAAGTAGGTCAACTTATAGGGAAAAATCC  
R R Q H D V E N K S Q V G Q L I G K N P

1021  
ACTTTTTTCAAAGTCAACTGTATCTAGAGAAAATAATCACTCTAGTCAAGGTGACTCTAA  
L F S K S T V S R E N N H S S Q G D S N  
1081

Fig. 6-1

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CAAACAGTCATTCTCTAAAAAAGTATCTCAGGTTACTAATGTAGCTAATAGACCGATGTT  
K Q S F S K K V S Q V T N V A N R P M L  
1141  
AACTAATAATTCTAGAACAATTTTCAGTGATAAATAAATTACCTAAAACAGGTGATGATCA  
T N N S R T I S V I N K L P K T G D D Q  
1201  
AAATGTCATTTTTTAAACTTGTAGGTTTTGGTTTAATTTTATTAACAAGTCTCTGCGGTTT  
N V I F K L V G F G L I L L T S L C G L  
1261  
GAGACGCAATGAAAATTAAGTATAATCAACCATTTAGTAACTATTATAATGATATATGCA  
R R N E N \*  
1321  
ATCAATAAAAAAGGAATCGAATACGAGATTCCTTTTTTATAATTAGGTTGGTTAGGGTGAC  
1381  
TTTTTTCATTTGGCTATTCTTGAAAGTTTATAAAAATGTAGTATAATAGTCACATTAAAA  
1441  
TGTTTTGAAAATATTGATGAACAACATCATCAAATAGAGGTCAT

Fig. 6-2

Inventor: Reinscheid et al.

App. No.: Unknown

Docket No.: 116676-006

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1  
GCATAAATAAGTCACAATTTCTTCTAAAAATTATGTCTTTACTTAACTTTAATTGAATA  
61  
TGCTACCATCACATTCTTTGTAAAATTTTAAATAACCTAGTTTCTGATGGTTTAGATGA  
121  
AGTATTAAAAATATACTATTATCTCATTGTAAATCCTAATGTTAGTATGACTATCTATCA  
181  
TGTTTTATAATATTGAAGGAAAATTTAAAAATATCATGTTTTAGATATCAACTATTTAAT  
241  
TTTAAACATACAAATTAATAATAAATTGCAATTAAATAACAAATTACCTTGACATAAATT  
301  
ATAAAATGATTTAATATATATAATCTAAATAAAAAATAATAAAATGACTTTTAAATT  
361  
TAAAAAAGTAAGGAGAAAATTAATTGTTCAATAAAATAGGTTTTAGAACTTGGAATCA  
421  
RBS M F N K I G F R T W K S  
GGAAAGCTTTGGCTTTATATGGGAGTGCTAGGATCAACTATTATTTTAGGATCAAGTCCT  
G K L W L Y M G V L G S T I I L G S S P  
481  
Repeat 1 (SEQ ID 83)  
GTATCTGCTATGGATAGTGTTGGAAATCAAAGTCAAGGTAATGTTCTAGAGCGTCGCCAA  
V S A M D S V G N Q S Q G N V L E R R Q  
541  
Repeat 2 (SEQ ID 84)  
CGTGATGCGGATAACAAGAGCCAAGGTAATGTTTTAGAGCGTCGCCAACGTGATGCAGAT  
R D A D N K S Q G N V L E R R Q R D A D  
601  
Repeat 3 (SEQ ID 85)  
AACAAAAGTCAGGCAATGTTCTAGAACGTCGCCAACGTGATGTTGATAACAAGAGCCAA  
N K S Q G N V L E R R Q R D V D N K S Q  
Repeat 4 (SEQ ID 86)  
GGTAACGTTCTAGAGCGTCGCCAACGCGATGCTGATAACAAGAGCCAAGGTAATGTTTTA  
G N V L E R R Q R D A D N K S Q G N V L  
721  
Repeat 6 (SEQ ID 88)  
GAGCGCCGCCAACGCGATGCAGATAACAAAAGTCAAGGTAATGTTCTAGAGCGTCGCCAA  
E R R Q R D A D N K S Q G N V L E R R Q  
781  
Repeat 7 (SEQ ID 89)  
CGCGATGTTGATAACAAGAGCCAGGGTAATGTTTTAGAGCGTCGCCAACGCGATGCAGAT  
R D V D N K S Q G N V L E R R Q R D A D  
841  
Repeat 8 (SEQ ID 90)  
AACAAAAGTCAGGTAATGTTTGTAGAGCGTCGCCAACGCGATGTTGATAACAAAAGCCAA  
N K S Q G N V L E R R Q R D V D N K S Q  
Repeat 9 (SEQ ID 91)  
GGTAATGTTTTAGAGCGTCGCCAACGTGATGCTGATAACAAAAGTCAGGGCAATGTTCTA  
G N V L E R R Q R D A D N K S Q G N V L  
961  
Repeat 11 (SEQ ID 93)  
GAGCGTCGCCAACGTGATGCGGATAACAAAAGCCAAGGTAATGTTCTAGAGCGTCGCCAA  
E R R Q R D A D N K S Q G N V L E R R Q  
1021  
Repeat 12 (SEQ ID 94)  
CGCGATGCGGATAACAAAAGTCAGGGCAATGTTTTAGAGCGTCGCCAACGTGATGCTGAT  
R D A D N K S Q G N V L E R R Q R D A D

Fig. 7-1

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1081  
AACAAAAGTCAAGGTAATGTTCTAGAGCGTCGCCAACGCGATGCAGATAACAAAAGCCAA  
N K S Q G N V L E R R Q R D A D N K S Q  
Repeat 13 (SEQ ID 95)  
Repeat 14 (SEQ ID 96)  
Repeat 15 (SEQ ID 97)  
GGTAATGTTCTAGAGCGTCGCCAACGCGATGCTGATAACAAAAGTCAAGGTAATGTTCTA  
G N V L E R R Q R D A D N K S Q G N V L  
1201  
Repeat 16 (SEQ ID 98)  
GAGCGTCGCCAACGTGATGCTGATAACAAGAGCCAAGGCAATGTTCTTGAGCGTCGTCAA  
E R R Q R D A D N K S Q G N V L E R R Q  
1261  
Repeat 17 (SEQ ID 99)  
CGCGATGTCGATAACAAAAGTCAGGGTAATGTTTTAGAGCGTCGCCAACGTGATGCGGAT  
R D V D N K S Q G N V L E R R Q R D A D  
1321  
Repeat 18 (SEQ ID 100)  
AACAAGAGTCAAGGTAATGTTTTAGAGCGTCGCCAACGCGATGCGGATAACAAGAGCCAA  
N K S Q G N V L E R R Q R D A D N K S Q  
Repeat 19 (SEQ ID 101)  
Repeat 20 (SEQ ID 102)  
GGTAATGTTTTAGAGCGTCGCCAACGCGATGCGGATAACAAGAGTCAAGGTAATGTTTTA  
G N V L E R R Q R D A D N K S Q G N V L  
1441  
Repeat 21 (SEQ ID 103)  
GAGCGTCGCCAACGCGATGCGGATAACAAGAGCCAAGGTAATGTTTTAGAGCGTCGCCAA  
E R R Q R D A D N K S Q G N V L E R R Q  
1501  
Repeat 22 (SEQ ID 104)  
CGCGATGCAGATAACAAAAGTCAAGGTAATGTTTTAGAGCGTCGCCAACGCGATGCTGAT  
R D A D N K S Q G N V L E R R Q R D A D  
1561  
Repeat 23 (SEQ ID 105)  
AACAAGAGCCAAGGTAATGTTTTAGAGCGTCGTCAACGTGATGCAGATAACAAAAGTCAG  
N K S Q G N V L E R R Q R D A D N K S Q  
Repeat 24 (SEQ ID 106)  
Repeat 25 (SEQ ID 107)  
GGCAATGTTTTAGAGCGTCGTCAACGTGATGCGGATAACAAGAGCCAAGGTAATGTTTTA  
G N V L E R R Q R D A D N K S Q G N V L  
1681  
Repeat 26 (SEQ ID 108)  
GAGCGTCGCCAACGTGATGCGGATAACAAGAGCCAGGGCAATGTTCTAGAACGTCGTCAA  
E R R Q R D A D N K S Q G N V L E R R Q  
1741  
Repeat 27 (SEQ ID 109)  
CGTGATGCGGATAACAAGAGCCAAGGTAACGTTTTAGAGCGTCGCCAACGTGATGCGGAT  
R D A D N K S Q G N V L E R R Q R D A D  
1801  
Repeat 28 (SEQ ID 110)  
AACAAGAGCCAGGGCAATGTTTTAGAGCGCGCCAACGCGATGCAGATAACAAAAGTCAA  
N K S Q G N V L E R R Q R D A D N K S Q  
Repeat 29 (SEQ ID 111)  
Repeat 30 (SEQ ID 112)  
GGTAATGTTCTAGAGCGTCGCCAACGCGATGCAGATAACAAGAGCCAGGGTAATGTTCTA  
G N V L E R R Q R D A D N K S Q G N V L  
1921  
GAGCGTCGCCAACGCGATGCGGAAAACAAAAGTCAAGTAGGTCAACTTATAGGGAAAAAT  
E R R Q R D A E N K S Q V G Q L I G K N  
1981

Fig. 7-2

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CCACTTTTTTCAAAGTCAACTGTATCTAGAGAAAATAATCACTCTAGTCAAGGTGACTCT  
P L F S K S T V S R E N N H S S Q G D S  
2041  
AACAAACAGTCATTCTCTAAAAAATATCTCAGGTTACTAATGTAGCTAATGGACCGATG  
N K Q S F S K K I S Q V T N V A N G P M  
2101  
TTAACTAATAATTCTAGAACAATTTTCAGTGATAAATAAATTACCTAAAACAGGTGATGAT  
L T N N S R T I S V I N K L P K T G D D  
2161  
CAAAATGTCATTTTTTAACTTGTAGGTTTTGGTTTAATTTTGTTAACAAGTCTCTGCGGT  
Q N V I F K L V G F G L I L L T S L C G  
2221  
TTGAGACGCAATGAAAATTAAGTATAATCAACCATTTAGTAACTATTATAATGATATATG  
L R R N E N \*  
2281  
CAATCAATAAAAAAGGAATCGAATACGAGATTCCTTTTTTATAATTAGGTTGGTTAGGGTG  
2341 2361 2381  
ACTTTTTTCATTTGGCTATTCTTGAAAGTTTATAAAAATGTAGTATAATAGTCACATTAA  
2401 2421 2441  
AATGTTTTGAAAATATTGATGAACAACATCATCAAATAGAGGTCAT

Fig. 7-3

Inventor: Reinscheid et al.

App. No.: Unknown

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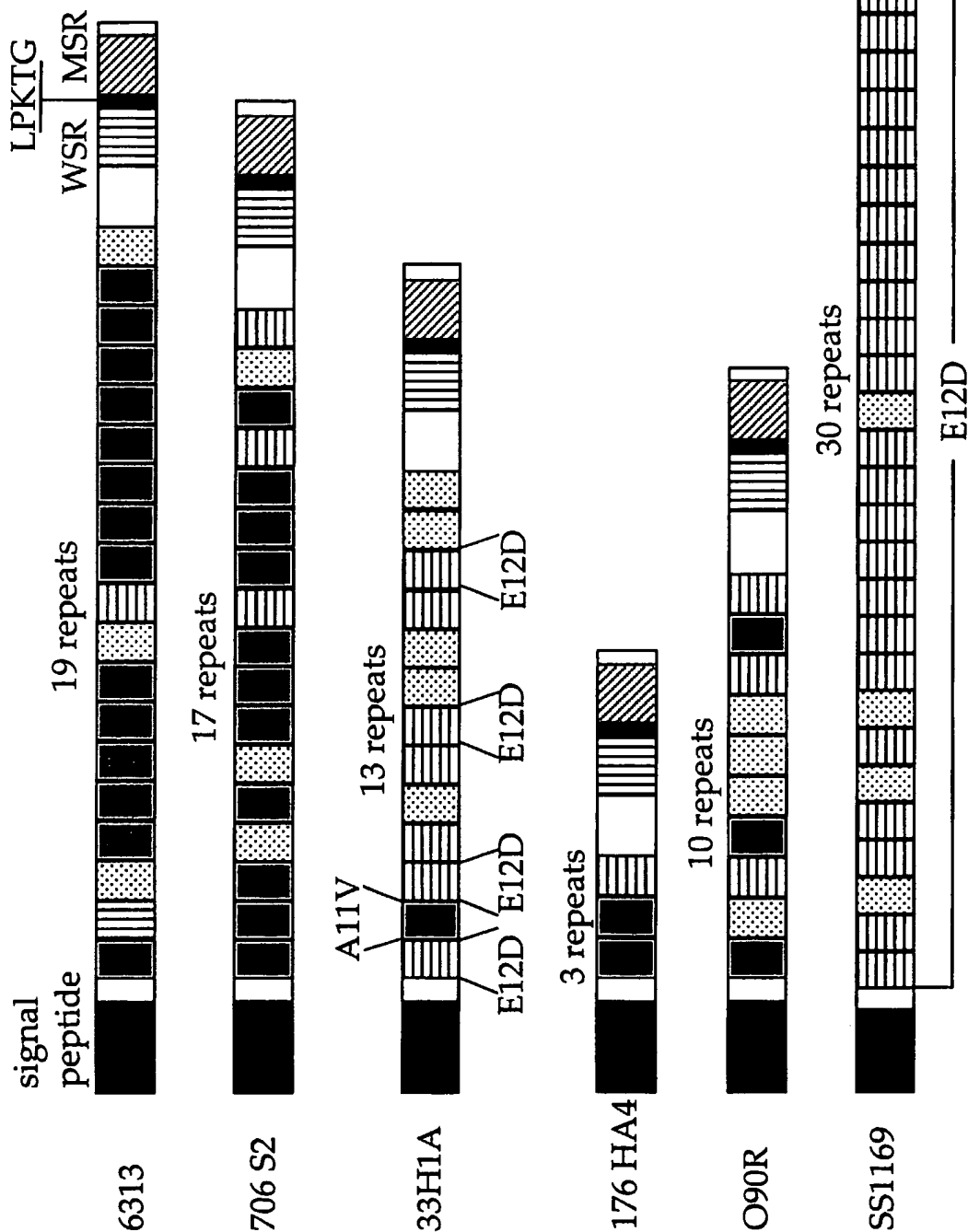


Fig. 8

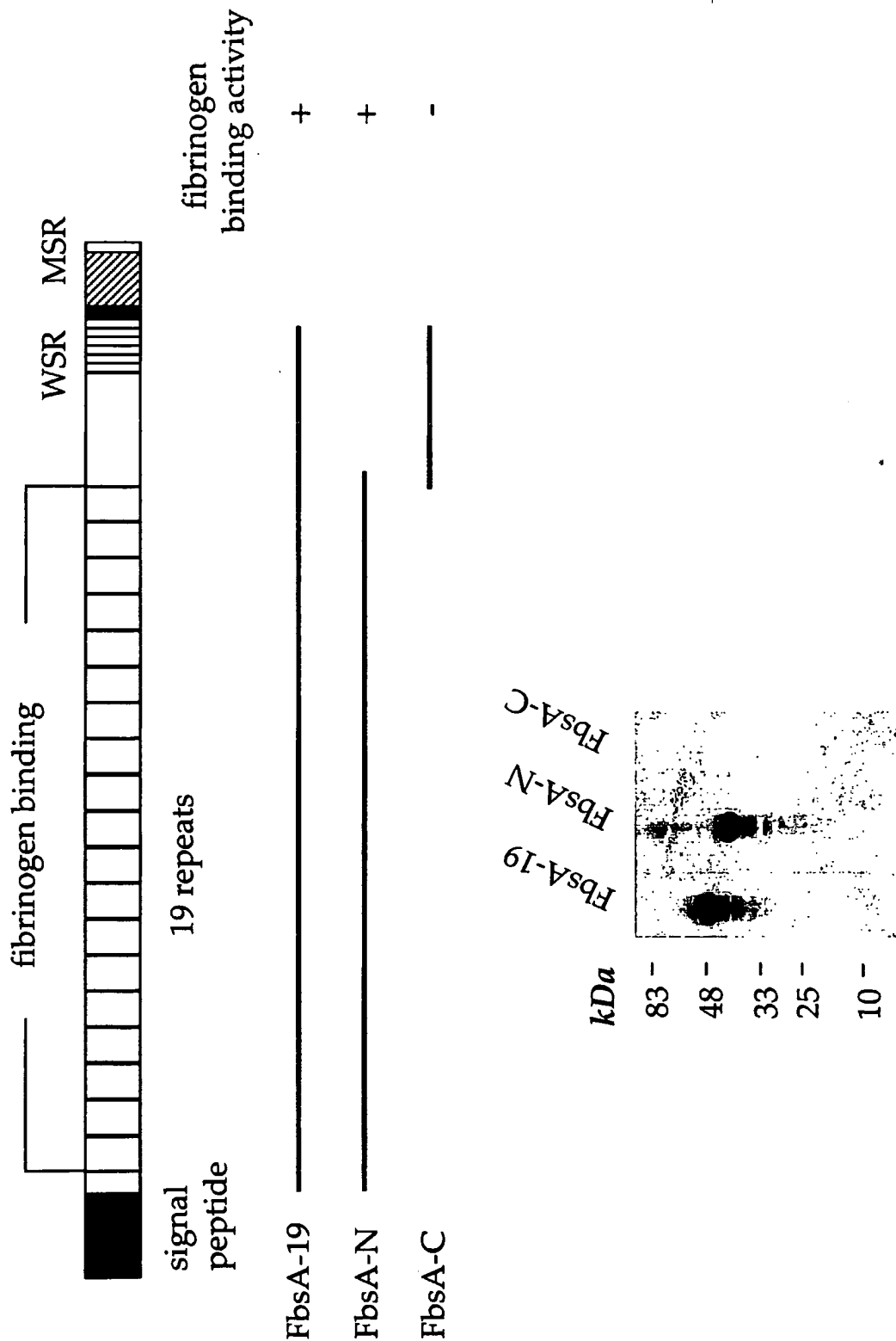


Fig. 9



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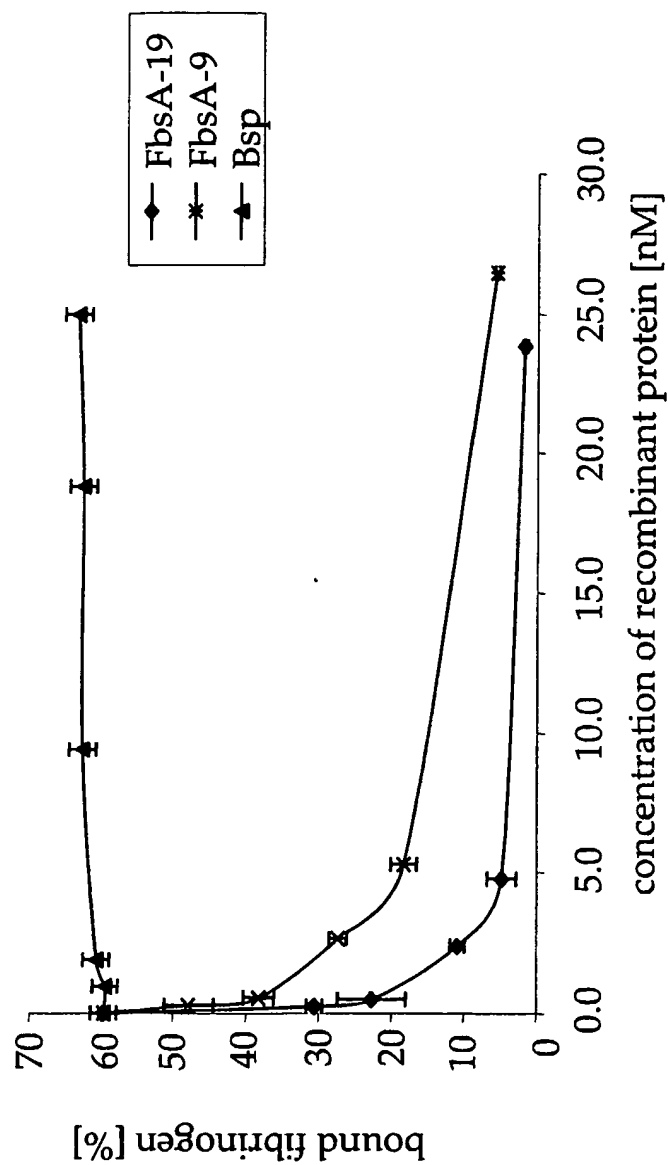



Fig. 10



GNVLERRQRDAENRSQ (SeqID 204)  
GLSONRDVRENQRARE (SeqID205)  
GNVLERRQRDAENRSQ  
GLSONRDVRENQRARE  
ANVLERRQRDAENRSQ (SeqID 206)  
GA<sub>V</sub>LERRQRDAENRSQ (SeqID 207)  
GN<sub>A</sub>LERRQRDAENRSQ (SeqID 208)  
GNV<sub>A</sub>ERRQRDAENRSQ (SeqID 209)  
GNVL<sub>A</sub>RRQRDAENRSQ (SeqID 210)  
GNVLE<sub>A</sub>RQRDAENRSQ (SeqID 211)  
GNVL<sub>E</sub>R<sub>A</sub>QRDAENRSQ (SeqID 212)  
GNVLERR<sub>A</sub>RDENRSQ (SeqID 213)  
GNVLERRQ<sub>A</sub>DAENRSQ (SeqID 214)  
GNVLERRQR<sub>A</sub>ENRSQ (SeqID 215)  
GNVLERRQRDAEN<sub>R</sub>RSQ (SeqID 216)  
GNVLERRQRDAEN<sub>A</sub>RSQ (SeqID 217)  
GNVLERRQRDAEN<sub>E</sub>ARSQ (SeqID 218)  
GNVLERRQRDAEN<sub>A</sub>SQ (SeqID 219)  
GNVLERRQRDAENR<sub>A</sub>Q (SeqID 220)  
GNVLERRQRDAENR<sub>S</sub>A (SeqID 221)  
GNVLERRQRDAENRSQ  
GLSONRDVRENQRARE  
GNVLERRQRDAENRSQ  
GLSONRDVRENQRARE

Fig. 11

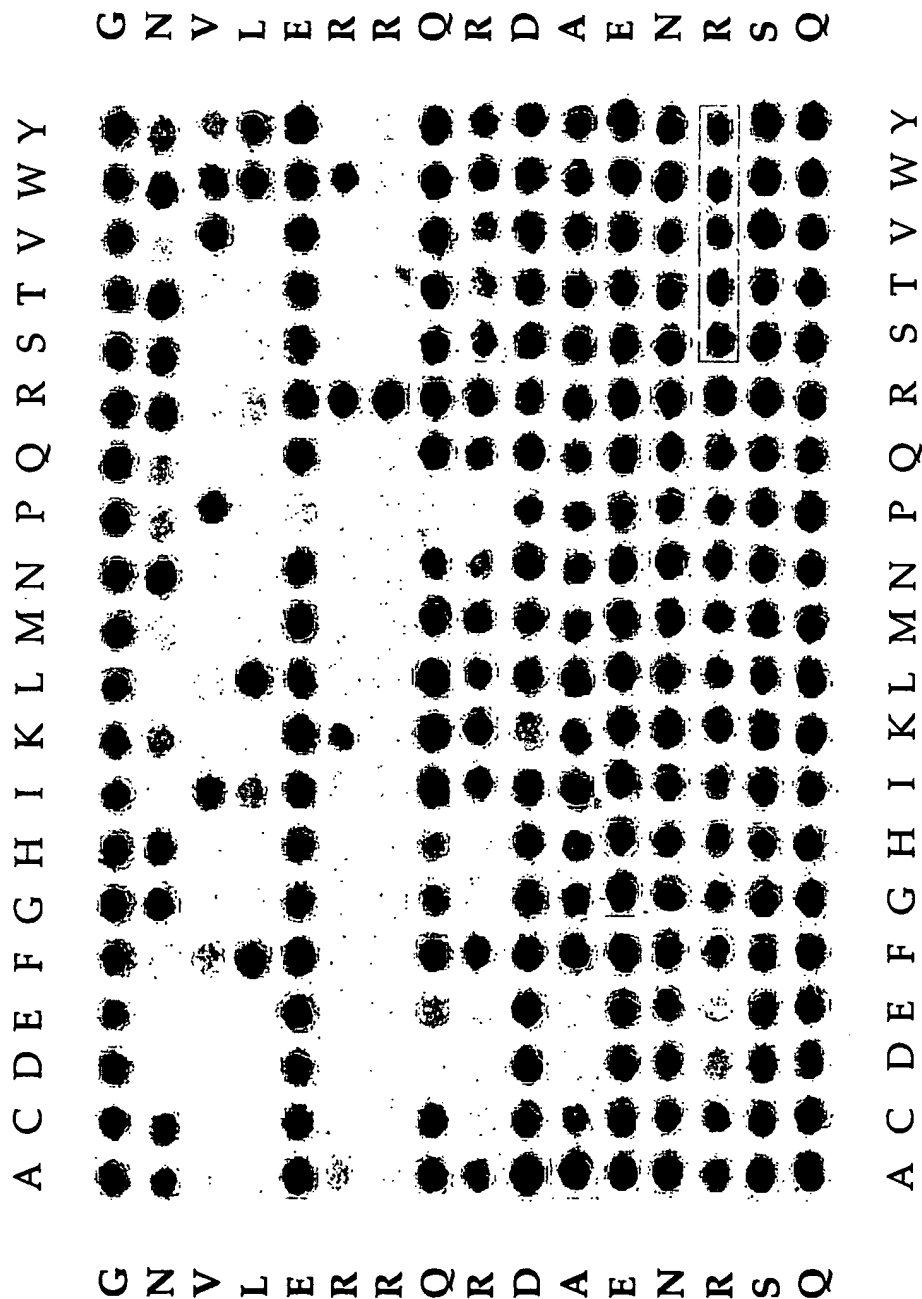


Fig. 12

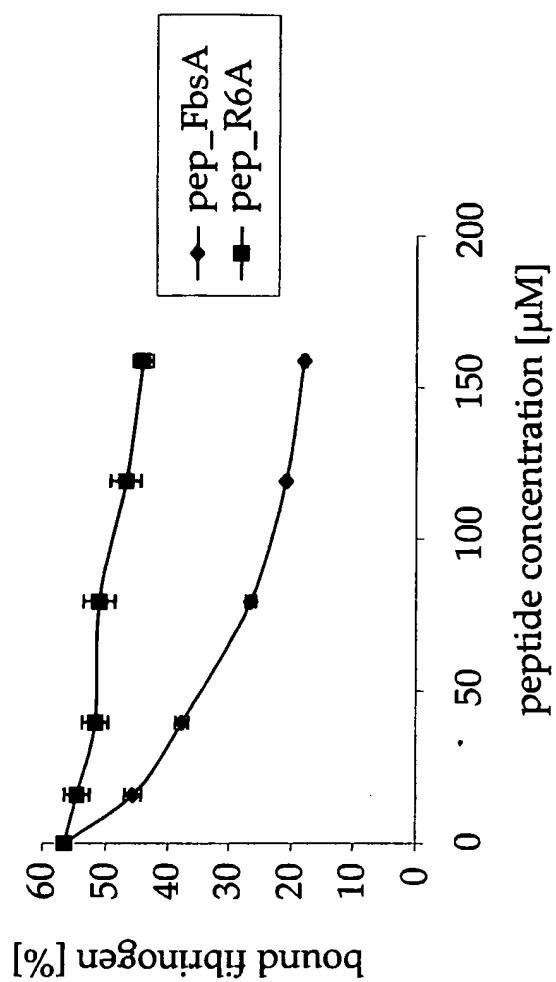


Fig. 13

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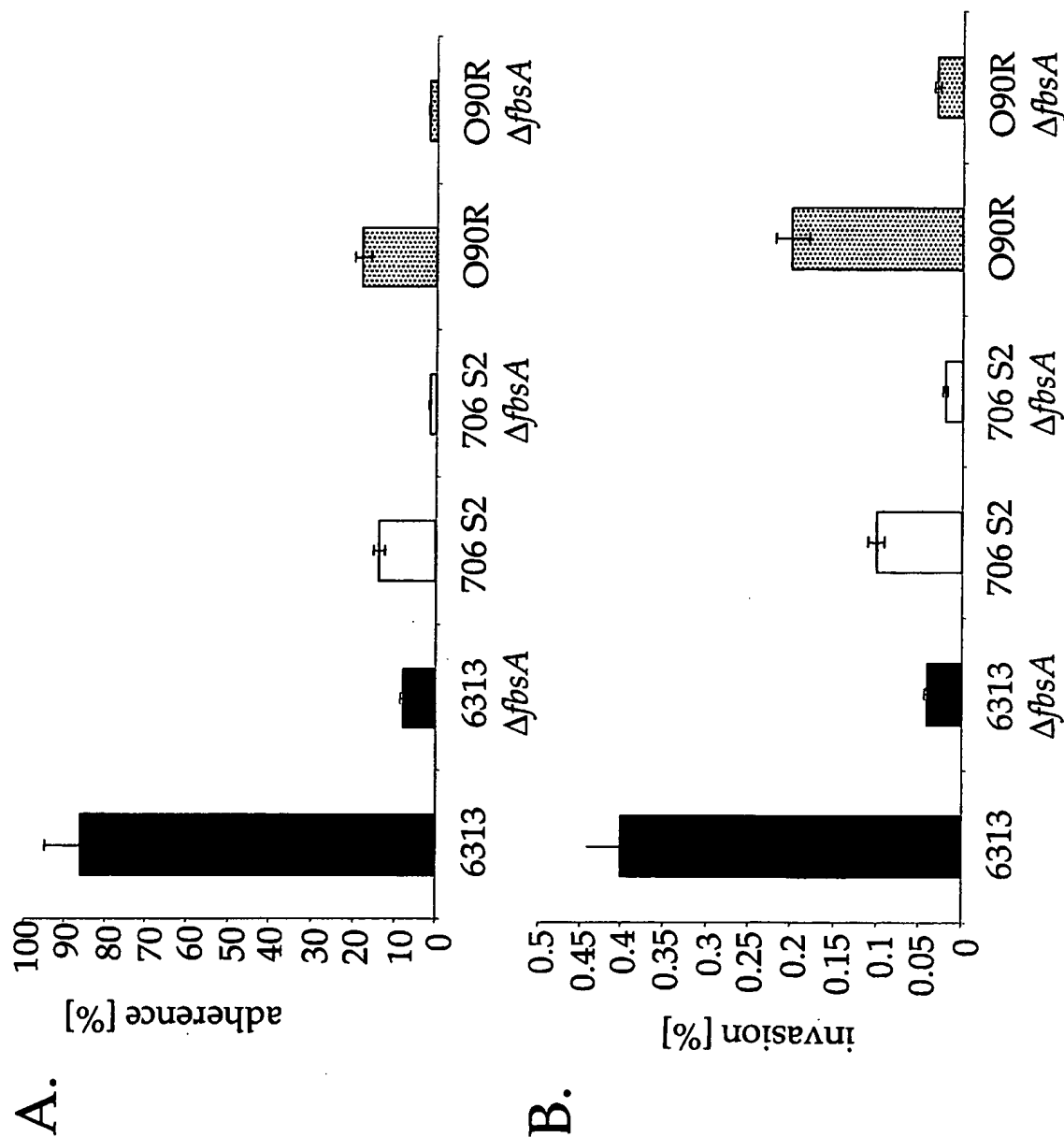


Fig. 14

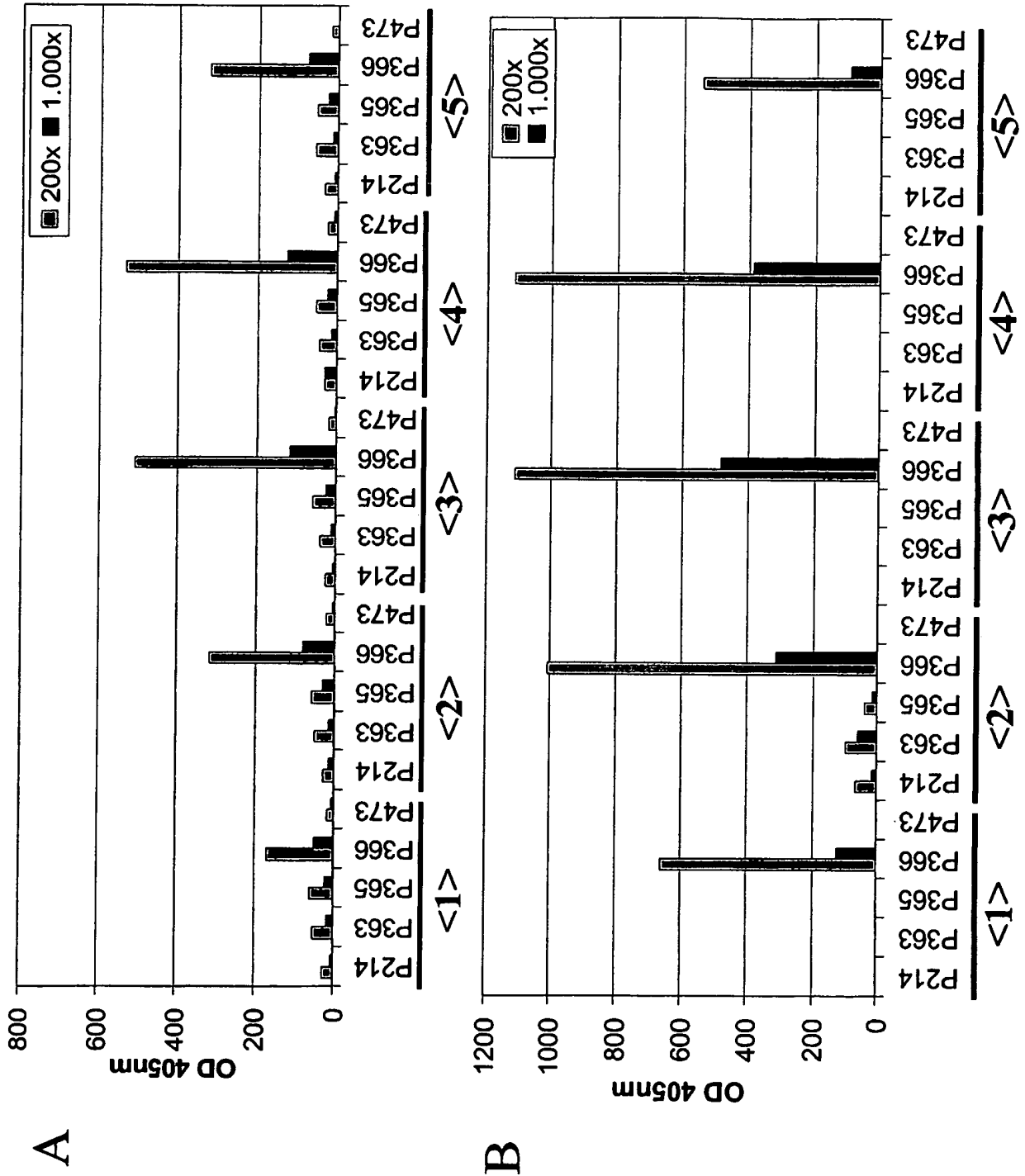


Fig. 15

1  
ATTTTAAAGCAATATTTTAAAACATAAAAAAAGAAAAATCAACTACTTAAGCTAATTGAA  
61  
GTATTTCTAAGATAATAAAAAATAAGATTATCAAATAAAAAGAAAAATCATTCAAAAATT  
121  
GGGAAAAAACTTTAAAATTCCATACCTTATAATAAGAAATTATTGATATCATAATAAGTG  
181  
ATAGTTTGTATATTCTAGGATATTCTGTATCTGATCTTAGATTTAGAAACGACATTTTCGG  
241  
CACAAATAGGAGTTGTAAAATGAGAAAATACCAAAAATTTTCTAAAATATTGACGTTAAGT  
301 RBS M R K Y Q K F S K I L T L S  
CTTTTTTGTGTGCGCAAATACCGCTTAATACCAATGTTTTAGGGGAAAGTACCGTACCG  
L F C L S Q I P L N T N V L G E S T V P  
361  
GAAATGGTGCTAAAGGAAAGTTAGTTGTAAAAAGACAGATGACCAGAACAAACCACTT  
E N G A K G K L V V K K T D D Q N K P L  
421  
TCAAAAGCTACCTTTGTTTTAAAACTACTGCTCATCCAGAAAGTAAAATAGAAAAAGTA  
S K A T F V L K T T A H P E S K I E K V  
481  
ACTGCTGAGCTAACAGGTGAAGCTACTTTTGATAATCTCATACCTGGAGATTATACTTTA  
T A E L T G E A T F D N L I P G D Y T L  
541  
TCAGAAGAAACAGCGCCCGAAGGTTATAAAAAGACTAACCAGACTTGGCAAGTTAAGGTT  
S E E T A P E G Y K K T N Q T W Q V K V  
601  
GAGAGTAATGGAAAACTACGATACAAAATAGTGGTGATAAAAATTCCACAATTGGACAA  
E S N G K T T I Q N S G D K N S T I G Q  
661  
AATCACGAAGAACTAGATAAGCAGTATCCCCCACAGGAATTTATGAAGATACAAAGGAA  
N H E E L D K Q Y P P T G I Y E D T K E  
721  
TCTTATAAACTTGAGCATGTAAAGGTTCAAGTTCCAAATGGAAAGTCAGAGGCCAAAAGCA  
S Y K L E H V K G S V P N G K S E A K A  
781  
GTTAACCCATATTCAAGTGAAGGTGAGCATATAAGAGAAATTCCAGAGGGAACATTATCT  
V N P Y S S E G E H I R E I P E G T L S  
841  
AAACGTATTTTCAAGTAGGTGATTTAGCTCATAATAAATATAAAATTGAGTTAACTGTC  
K R I S E V G D L A H N K Y K I E L T V  
901  
AGTGGA AAAACCATAGTAAAACAGTGGACAAACAAAGCCGTTAGATGTTGTCTTCGTA  
S G K T I V K P V D K Q K P L D V V F V  
961  
CTCGATAATTCTAACTCAATGAATAACGATGGCCCAAATTTTCAAAGGCATAATAAAGCC  
L D N S N S M N N D G P N F Q R H N K A  
1021

Fig. 16-1

AAGAAAGCTGCCGAAGCTCTTGGGACCGCAGTAAAAGATATTTTAGGAGCAAACAGTGAT  
K K A A E A L G T A V K D I L G A N S D  
1081  
AATAGGGTTGCATTAGTTACCTATGGTTCAGATATTTTTGATGGTAGGAGTGTAGATGTC  
N R V A L V T Y G S D I F D G R S V D V  
  
1141  
GTAAAAGGATTTAAAGAAGATGATAAATATTATGGCCTTCAAACCTAAGTTCACAATTCAG  
V K G F K E D D K Y Y G L Q T K F T I Q  
1201  
ACAGAGAATTATAGTCATAAACAATTAACAAATAATGCTGAAGAGATTATAAAAAGGATT  
T E N Y S H K Q L T N N A E E I I K R I  
1261  
CCTACAGAAGCTCCTAGAGCTAAATGGGGATCAACTACAAACGGACTTACTCCAGAGCAA  
P T E A P R A K W G S T T N G L T P E Q  
1321  
CAAAAGCAGTACTATCTTAGTAAAGTAGGGGAAACATTTACTATGAAAGCCTTCATGGAG  
Q K Q Y Y L S K V G E T F T M K A F M E  
1381  
GCAGATGATATTTTGAGTCAAGTAGATCGAAATAGTCAAAAAATTATTGTTTCATATAACT  
A D D I L S Q V D R N S Q K I I V H I T  
1441  
GATGGTGTTCACAAGATCATATGCTATTAATAATTTTAAATTGGGTGCATCATATGAA  
D G V P T R S Y A I N N F K L G A S Y E  
1501  
AGCCAATTTGAACAAATGAAAAAAATGGATATCTAAATAAAAGTAATTTTCTACTTACT  
S Q F E Q M K K N G Y L N K S N F L L T  
1561  
GATAAGCCCGAGGATATAAAAGGAAATGGGGAGAGTTACTTTTTGTTTCCCTTAGATAGT  
D K P E D I K G N G E S Y F L F P L D S  
1621  
TATCAAACACAGATAATCTCTGGAAACTTACAAAACTTCATTATTTAGATTTAAATCTT  
Y Q T Q I I S G N L Q K L H Y L D L N L  
1681  
AATTACCTAAAGGTACAATTTATCGAAATGGACCAGTAAGAGAACATGGAACACCAACC  
N Y P K G T I Y R N G P V R E H G T P T  
1741  
AAACTTTATATAAATAGTTTAAAACAGAAAAATTATGACATCTTTAATTTTGGTATAGAT  
K L Y I N S L K Q K N Y D I F N F G I D  
1801  
ATATCTGCTTTTAGACAAGTTTATAATGAGGATTATAAGAAAAATCAAGATGGTACTTTT  
I S A F R Q V Y N E D Y K K N Q D G T F  
1861  
CAAAAATTGAAAGAGGAAGCTTTTGAACCTTTCAGATGGGGAAATAACAGAACTAATGAAG  
Q K L K E E A F E L S D G E I T E L M K  
1921  
TCATTCTCTTCTAAACCTGAGTATTATACCCCGATAGTAACTTCATCCGATGCATCTAAC  
S F S S K P E Y Y T P I V T S S D A S N  
1981



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AATGAAATTTTATCTAA<sup>^</sup>AATTCAGCAACAATTTGAAAAGGTTTTAACAAAAGAAA<sup>^</sup>ACTCA  
N E I L S K I Q Q Q F E K V L T K E N S  
2041

ATTGTTAATGGA<sup>^</sup>ACTATAGAAGATCCTATGGGTGACAAAATCAATTTACAGCTTGGCAAC  
I V N G T I E D P M G D K I N L Q L G N  
2101

GGACAAACATTGCAACCAAGTGATTATACTTTACAGGGAAATGATGGAAGTATAATGAAA  
G Q T L Q P S D Y T L Q G N D G S I M K  
2161

GATAGCATTGCAACTGGTGGGCCTAATAATGATGGTGAATACTTAAAGGGGTAAATTA  
D S I A T G G P N N D G G I L K G V K L  
2221

GAATACATCAAAAATAAACTCTACGTTAGAGGTTTGAACTTAGGGGAGGGACAAAAGTA  
E Y I K N K L Y V R G L N L G E G Q K V  
2281

ACACTCACATATGATGTGAAACTAGATGACAGTTTTATAAGTAACAAATTCTATGACACT  
T L T Y D V K L D D S F I S N K F Y D T  
2341

AATGGTAGAACAACATTGAATCCTAAATCAGAGGATCCTAATACACTTAGAGATTTTCCA  
N G R T T L N P K S E D P N T L R D F P  
2401

ATCCCTAAAATTCGTGATGTGAGAGAATATCCTACAATAACGATTAAAAACGAGAAGAAG  
I P K I R D V R E Y P T I T I K N E K K  
2461

TTAGGTGAAATTGAATTTACAAAAGTTGATAAAGATAATAATAAGTTGCTTCTCAAAGGA  
L G E I E F T K V D K D N N K L L L K G  
2521

GCTACGTTTGAACTTCAAGAATTTAATGAAGATTATAAACTTTATTTACCAATAAAAAAT  
A T F E L Q E F N E D Y K L Y L P I K N  
2581

AATAATTCAAAAGTAGTGACGGGAGAAAACGGCAAAATTTCTTACAAAGATTTGAAAGAT  
N N S K V V T G E N G K I S Y K D L K D  
2641

GGCAAATATCAGTTAATAGAAGCAGTTTCGCCGAAGGATTATCAAAAAATTACTAATAAA  
G K Y Q L I E A V S P K D Y Q K I T N K  
2701

CCAATTTTAACTTTTGAAGTTGTAAAGGATCGATACAAAATATAATAGCTGTTAATAAA  
P I L T F E V V K G S I Q N I I A V N K  
2761

CAGATTTCTGAATATCATGAGGAAGGTGACAAGCATTTAATTACCAACACGCATATTCCA  
Q I S E Y H E E G D K H L I T N T H I P  
2821

CCAAAAGGAATTATTCGGATGACAGGTGGGAAAGGAATTCTATCTTTCATTTTAATAGGT  
P K G I I P M T G G K G I L S F I L I G  
2881

GGATCTATGATGTCTATTGCAGGTGGAATTTATATTTGGAAAAGATATAAGAAATCTAGT  
G S M M S I A G G I Y I W K R Y K K S S  
2941

Fig. 16-3

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GATATATCTAGAGAAAAAGATTAAGAATCATGTGTTTTAGTATTCTTAATTAATTAAATA  
D I S R E K D \*  
3001  
TAATTCGAAAGGAGTGGTGCTGCGGTAATATTATAATCCGTATATTATTATCTATGTTGA  
3061  
TTAACTAGAATAAGAAGGAGATAGAAATGAAAAAATCAACAAATGTCTTACAGTGTCT  
3121 RBS M K K I N K C L T V F  
CGACACTGCTATTGATCTTAACGTCACTATTCTCAGTTGCACCAGCGTTTGC GGACGACG  
S T L L L I L T S L F S V A P A F A D D  
3181  
TAACAACTGATACTGTGACCTTGCACAAGATTGTGATGCCACAAGCTGCATTTGATAACT  
V T T D T V T L H K I V M P Q A A F D N  
3241  
TTACTGAAGGTACAAAAGGTAAGAATGATAGCGATTATGTTGGTAAACAAATTAATGACC  
F T E G T K G K N D S D Y V G K Q I N D  
3301  
TTAAATCTTATTTTGGCTCAACCGATGCTAAAGAAATTAAGGGTGCTTCTTTGTTTTC  
L K S Y F G S T D A K E I K G A F F V F  
3361  
AAAATGAACTGGTACAAAATTCATTACTGAAAATGGTAAGGAAGTCGATACTTTGGAAG  
K N E T G T K F I T E N G K E V D T L E  
3421  
CTAAAGATGCTGAAGGTGGTGCTGTTCTTTCAGGGTTAACAAAAGACACTGGTTTTGCTT  
A K D A E G G A V L S G L T K D T G F A  
3481  
TTAACACTGCTAAGTTAAAAGGAACTTACCAAATCGTTGAATTGAAAGAAAAATCAAAC  
F N T A K L K G T Y Q I V E L K E K S N  
3541  
ACGATAACAACGGTTCTATCTTGGCTGATTCAAAAGCAGTTCCAGTTAAATCACTCTGC  
Y D N N G S I L A D S K A V P V K I T L  
3601  
CATTGGTAAACAACCAAGGTGTTGTTAAAGATGCTCACATTTATCCAAAGAATACTGAAA  
P L V N N Q G V V K D A H I Y P K N T E  
3661  
CAAAACCACAAGTAGATAAGAACTTTGCAGATAAAGATCTTGATTATACTGACAACCGAA  
T K P Q V D K N F A D K D L D Y T D N R  
3721  
AAGACAAAGGTGTTGTCTCAGCGACAGTTGGTGACAAAAAGAATACATAGTTGGAACAA  
K D K G V V S A T V G D K K E Y I V G T  
3781  
AAATTCTTAAAGGCTCAGACTATAAGAACTGGTTTGGACTGATAGCATGACTAAAGGTT  
K I L K G S D Y K K L V W T D S M T K G  
3841  
TGACGTTCAACAACAACGTTAAAGTAACATTGGATGGTAAAGATTTTCTGTTTTAAACT  
L T F N N N V K V T L D G K D F P V L N  
3901  
ACAAACTCGTAACAGATGACCAAGGTTTCCGTCTTGCCTTGAATGCAACAGGTCTTGCAG  
Y K L V T D D Q G F R L A L N A T G L A  
3961

Fig. 16-4

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CAGTAGCAGCTGCTGCAAAAGACAAAGATGTTGAAATCAAGATCACTTACTCAGCTACGG  
A V A A A A K D K D V E I K I T Y S A T  
4021  
TGAACGGCTCCACTACTGTTGAAGTTCCAGAAACCAATGATGTTAAATTGGACTATGGTA  
V N G S T T V E V P E T N D V K L D Y G  
4081  
ATAACCCAACGGAAGAAAGTGAACCACAAGAAGGTACTCCAGCTAACCAAGAAATTAAAG  
N N P T E E S E P Q E G T P A N Q E I K  
4141  
TCATTAAAGACTGGGCAGTAGATGGTACAATTACTGATGTTAATGTTGCAGTTAAAGCTA  
V I K D W A V D G T I T D V N V A V K A  
4201  
TCTTTACCTTGCAAGAAAAACAAACGGATGGTACATGGGTGAACGTTGCTTCACACGAAG  
I F T L Q E K Q T D G T W V N V A S H E  
4261  
CAACAAAACCATCACGCTTTGAACATACTTTCACAGGTTTGGATAATACTAAAACCTTACC  
A T K P S R F E H T F T G L D N T K T Y  
4321  
GCGTTGTGCAACGTGTTAGCGGCTACACTCCAGAATATGTATCATTTAAAAATGGTGTG  
R V V E R V S G Y T P E Y V S F K N G V  
4381  
TGACTATCAAGAACAACAAAACTCAAATGATCCAACCTCCAATCAACCCATCAGAACCAA  
V T I K N N K N S N D P T P I N P S E P  
4441  
AAGTGGTGACTTATGGACGTAAATTTGTGAAAACAAATCAAGCTAACACTGAACGCTTGG  
K V V T Y G R K F V K T N Q A N T E R L  
4501  
CAGGAGCTACCTTCCTTGTTAAGAAAGAAGGAAAATACTTGGCACGTAAAGCAGGTGCAG  
A G A T F L V K K E G K Y L A R K A G A  
4561  
CAACTGCTGAAGCAAAGGCAGCTGTAAAACTGCTAAACTAGCATTGGATGAAGCTGTTA  
A T A E A K A A V K T A K L A L D E A V  
4621  
AAGCTTATAACGACTTGACTAAAGAAAAACAAGAAGGCCAAGAAGGTAAAACAGCATTGG  
K A Y N D L T K E K Q E G Q E G K T A L  
4681  
CTACTGTTGATCAAAAACAAAAGCTTACAATGACGCTTTTGTTAAAGCTAACTACTCAT  
A T V D Q K Q K A Y N D A F V K A N Y S  
4741  
ATGAATGGGTTGCAGATAAAAAGGCTGATAATGTTGTTAAATTGATCTCTAACGCCGGTG  
Y E W V A D K K A D N V V K L I S N A G  
4801  
GTCAATTTGAAATTACTGGTTTGGATAAAGGCACTTATAGCTTGAAGAAACTCAAGCAC  
G Q F E I T G L D K G T Y S L E E T Q A  
4861  
CAGCAGGTTATGCGACATTGTCAGGTGATGTAACTTTGAAGTAACTGCCACATCATATA  
P A G Y A T L S G D V N F E V T A T S Y  
4921

GCAAAGGGGCTACAACGTGACATCGCATATGATAAAGGATCTGTAAAAAAGATGCCCAAC  
S K G A T T D I A Y D K G S V K K D A Q  
4981  
AAGTTCAAACAAAAAAGTAACCATCCCACAAACAGGTGGTATTGGTACAATTCTTTTCA  
Q V Q N K K V T I P Q T G G I G T I L F  
5041  
CAATTATTGGTTTAAAGCATTATGCTTGGAGCAGTAGTTGTCATGAAAAACGTCAATCAG  
T I I G L S I M L G A V V V M K K R Q S  
5101  
AGGAAGCTTAAGGCTAGTCTTTGATGGTGTATAAGCACAGTTAAAGCTGTGCTTATGATC  
E E A \*  
5161  
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Fig. 16-6

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1

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61  
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481 RBS  
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541 M K K Q F L K S A A I L S L A V T A  
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961  
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1081  
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E V V K D Y E N T I R Q I L S K K H E I  
1141

Fig. 17-1

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1201

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1261

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1381

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1681

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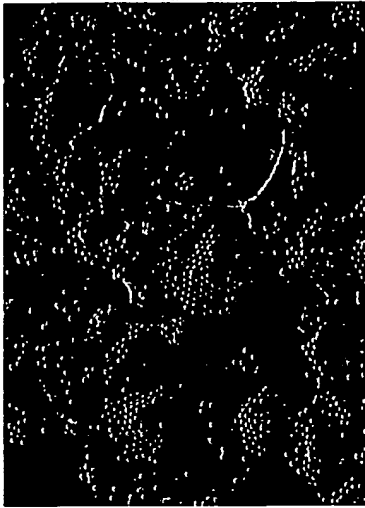
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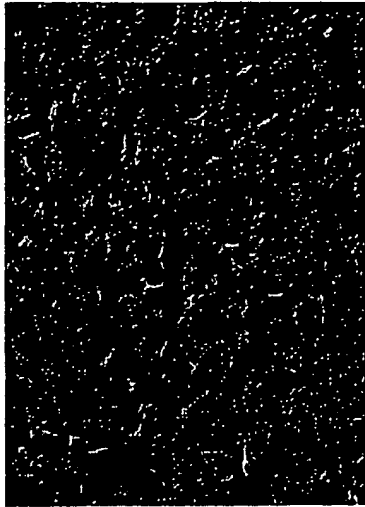
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2581  
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2641  
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2701  
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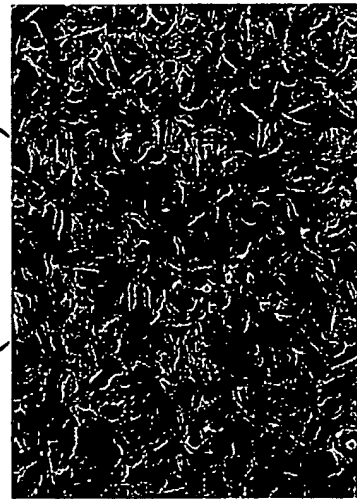
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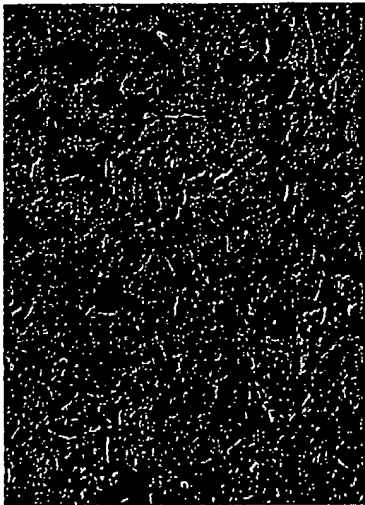
PabB



BSA (control)



PabA



PabD

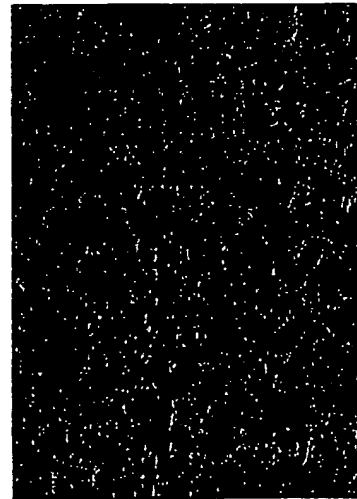


Fig. 18



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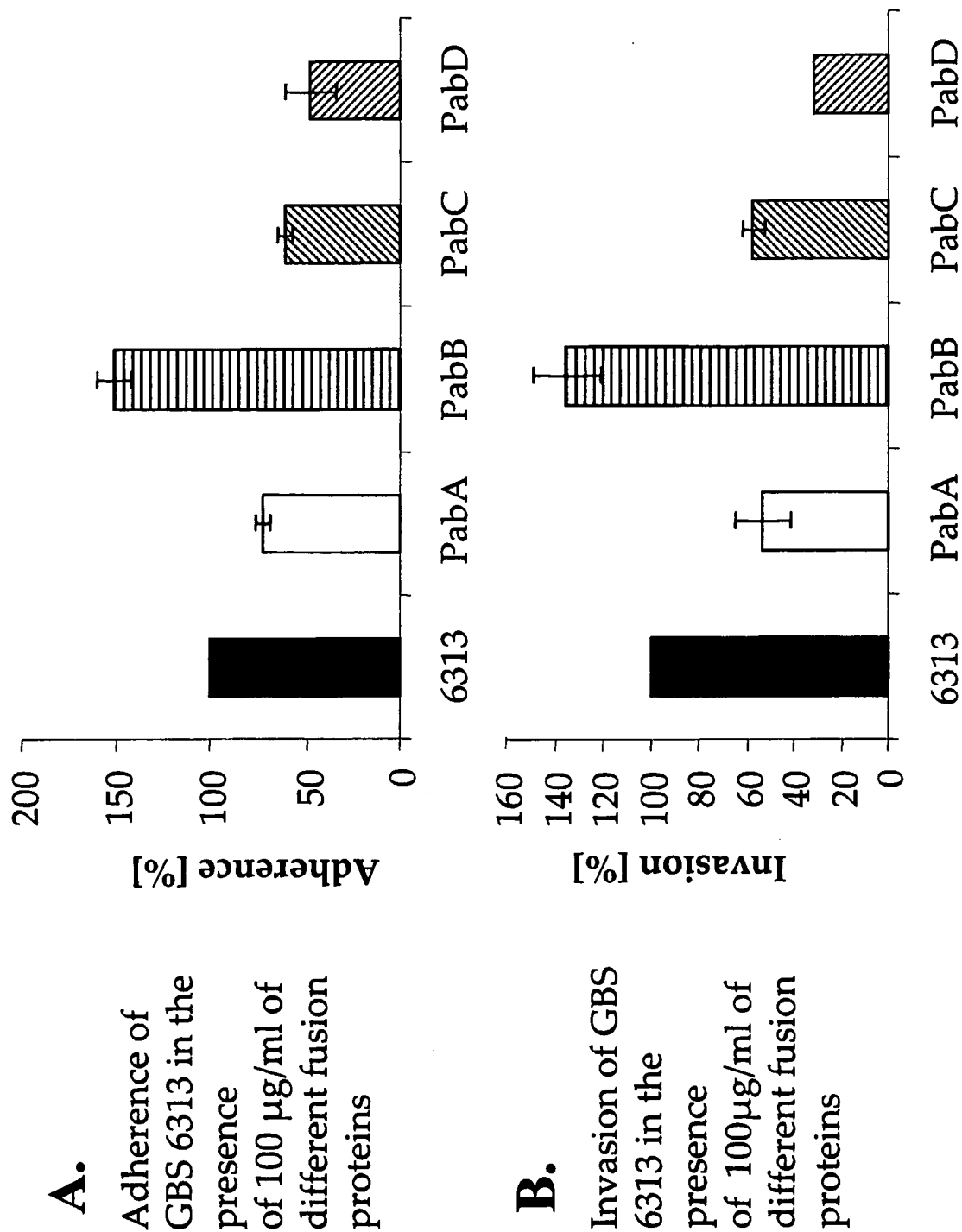


Fig. 19



Fig. 20

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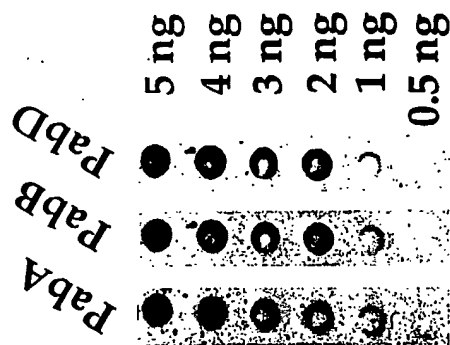


Fig. 21

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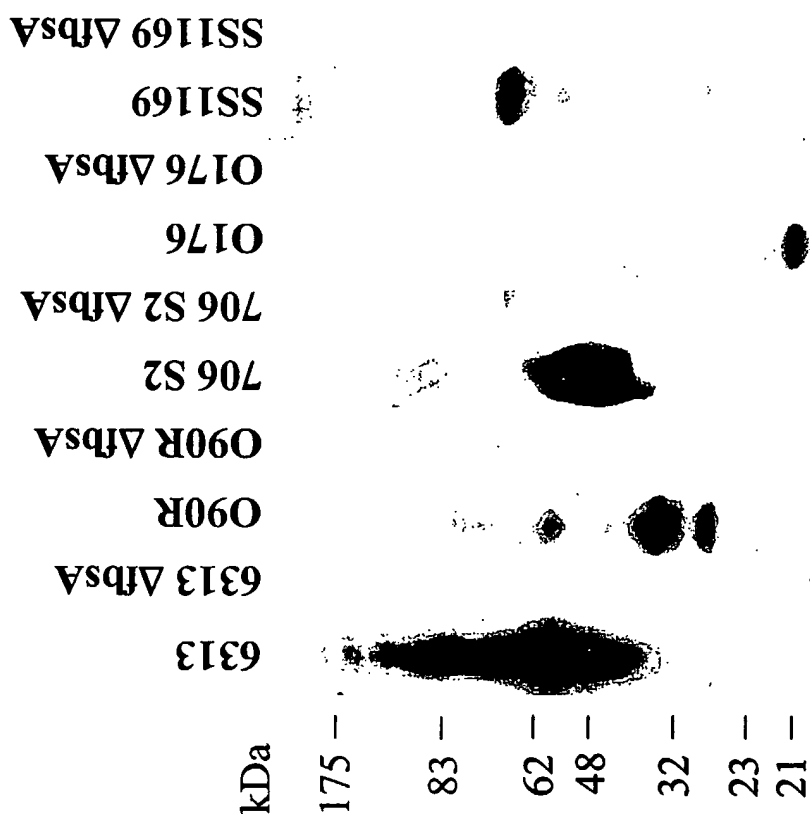


Fig. 22

Inventor: Reinscheid et al.

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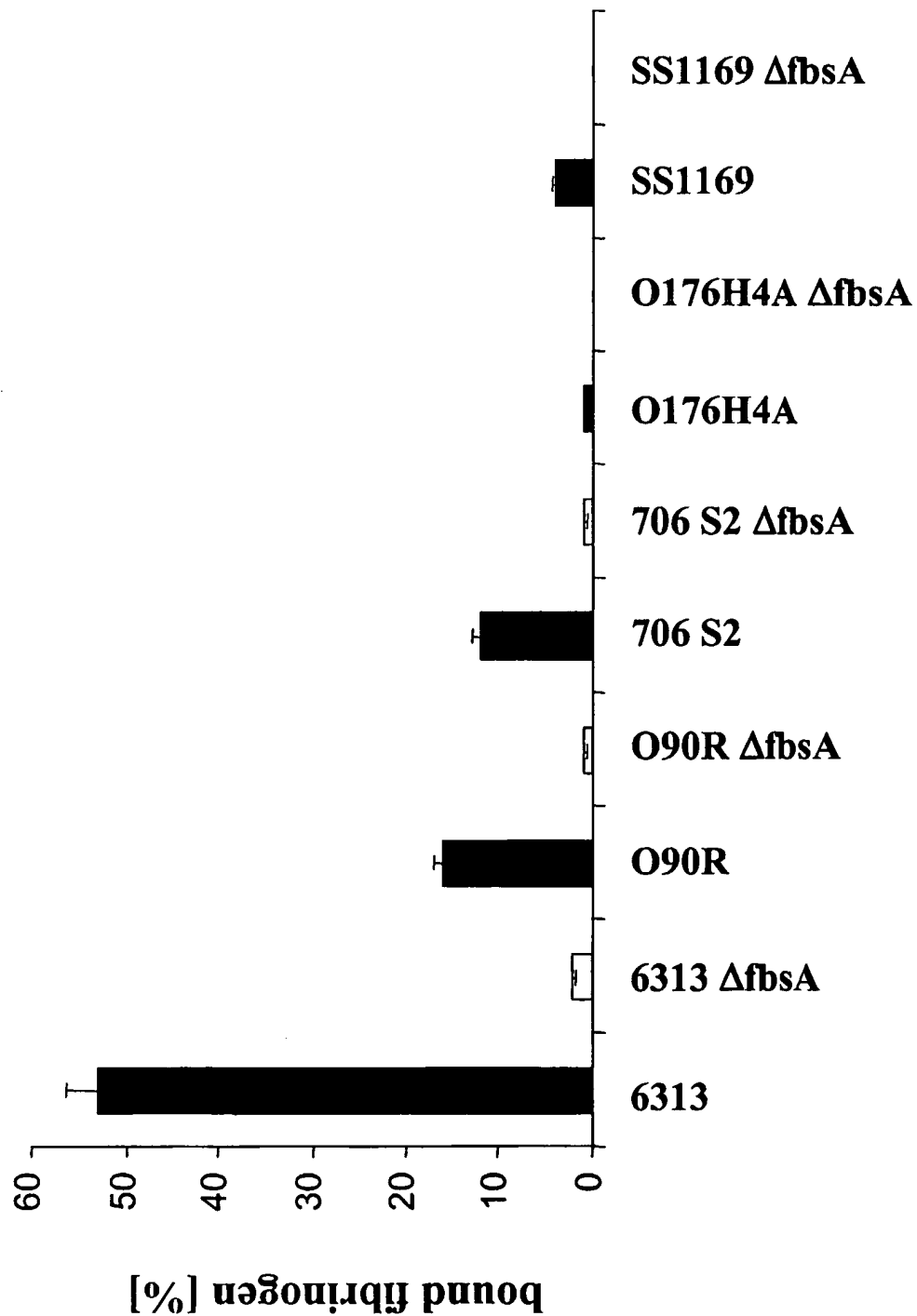


Fig. 23

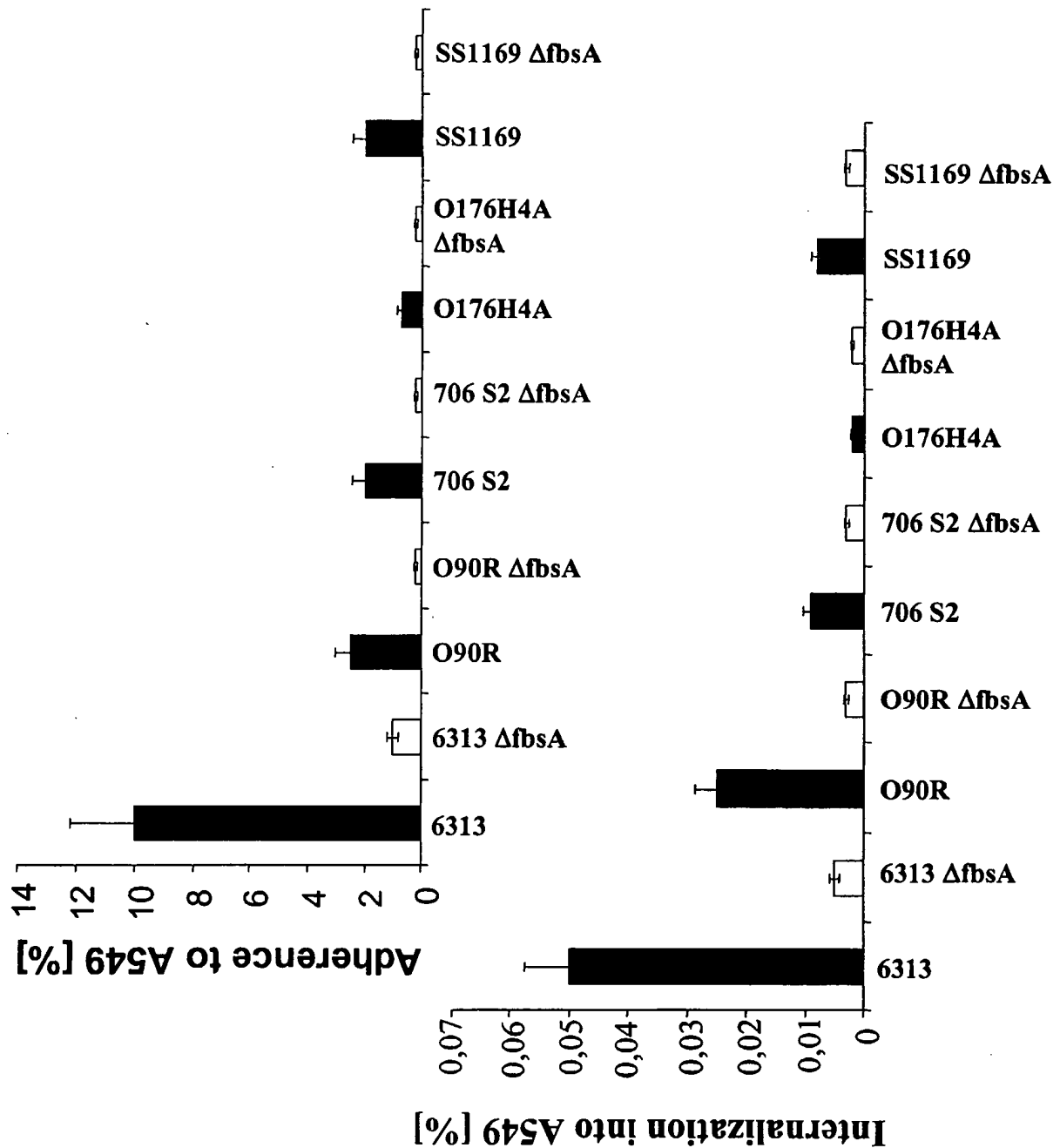


Fig. 24

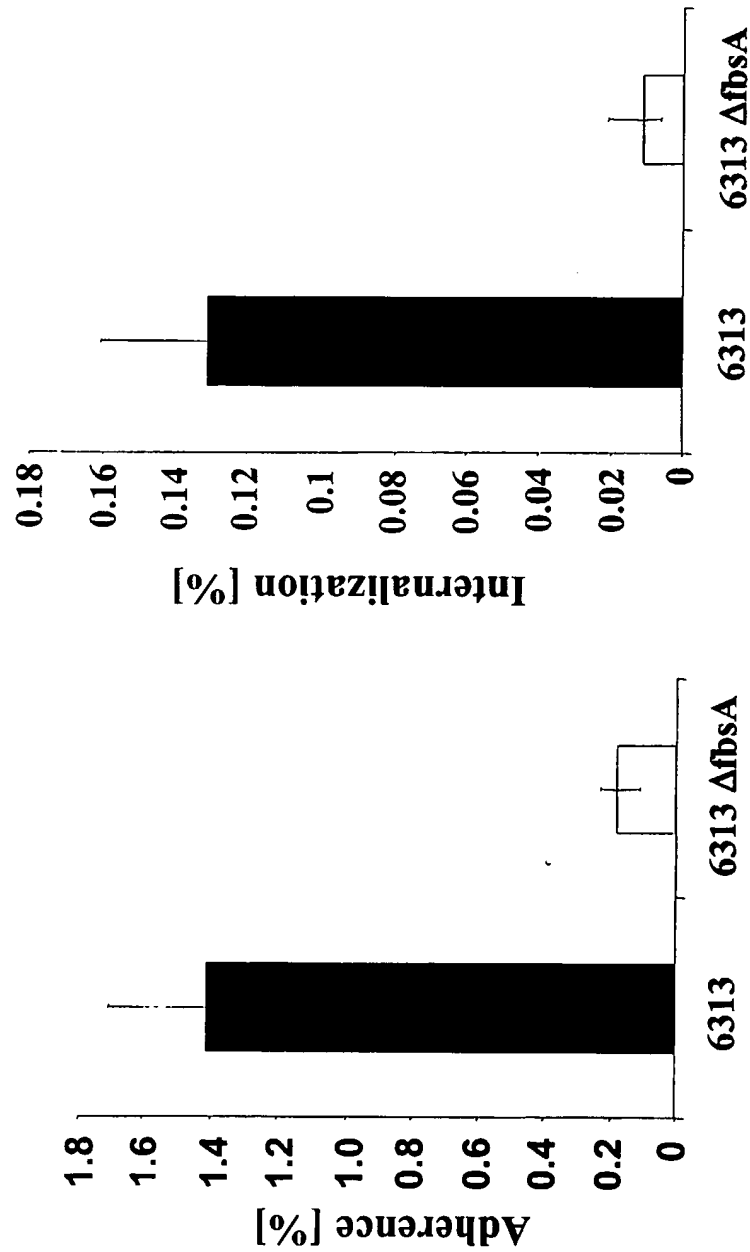


Fig. 25

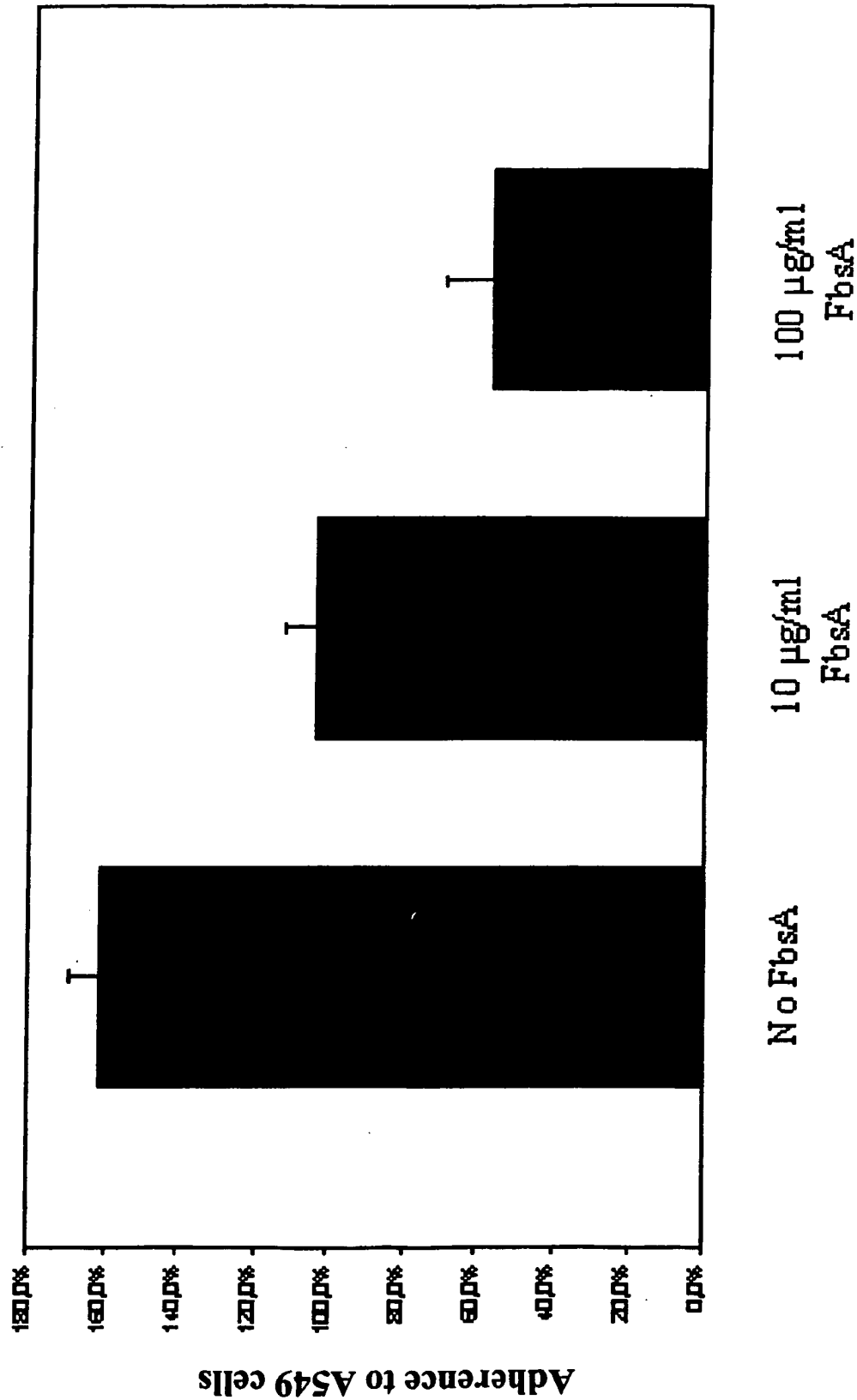


Fig. 26



Inventor: Reinscheid et al.

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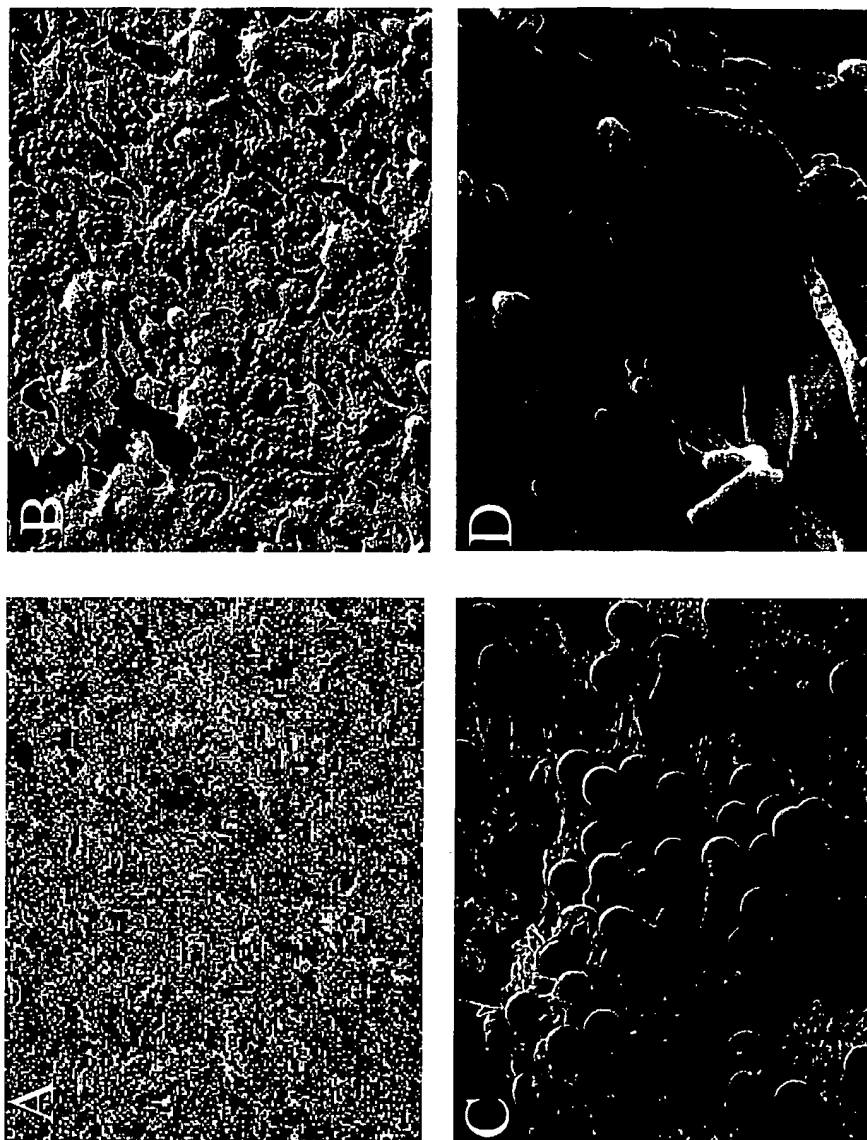


Fig. 27

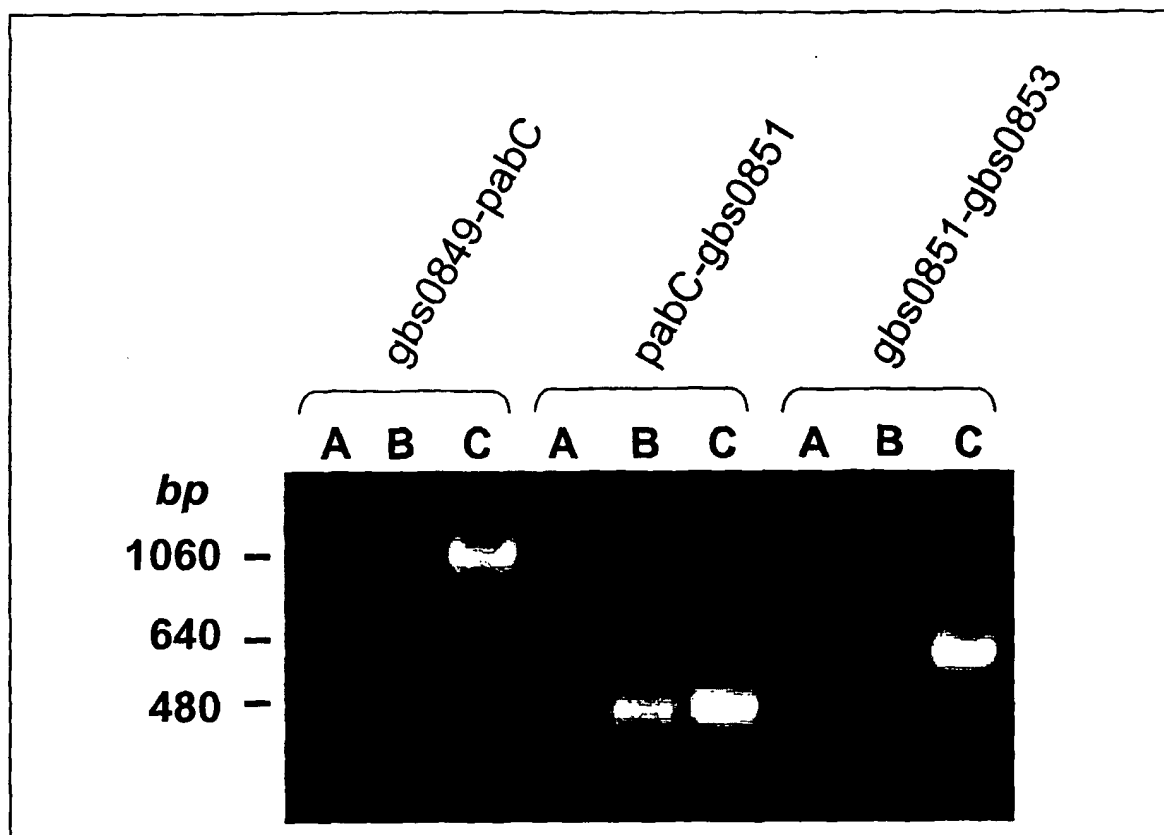


Fig. 28

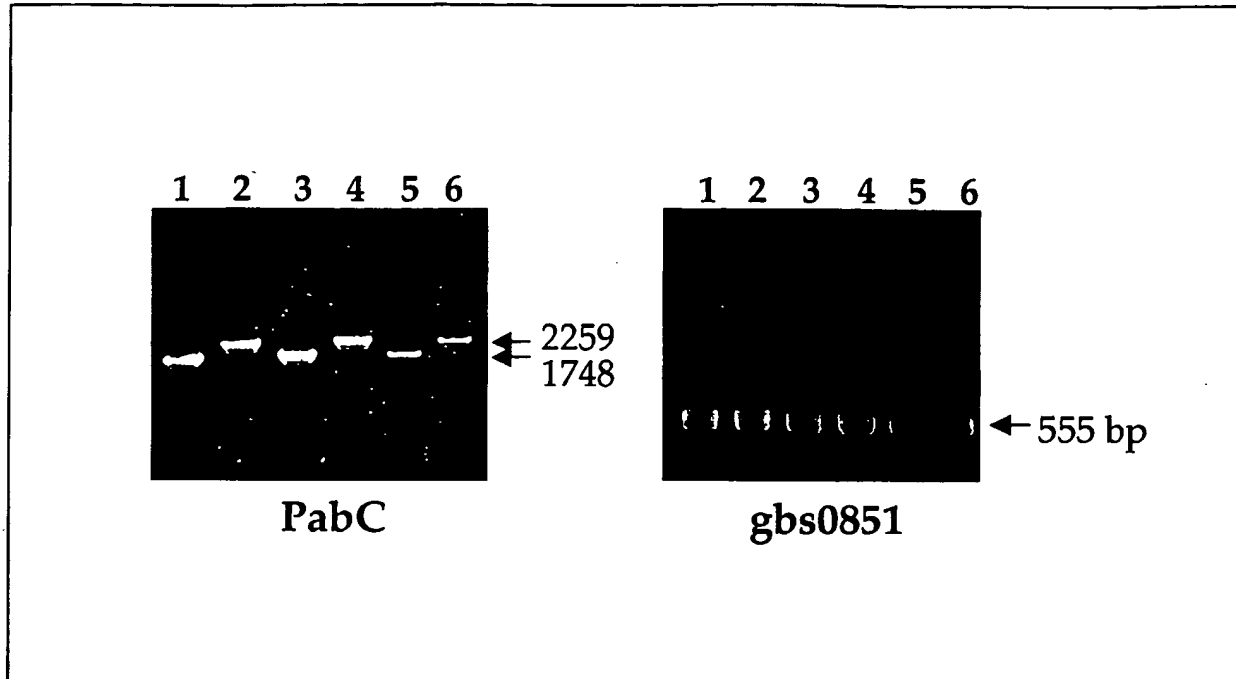


Fig. 29

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Fig. 30

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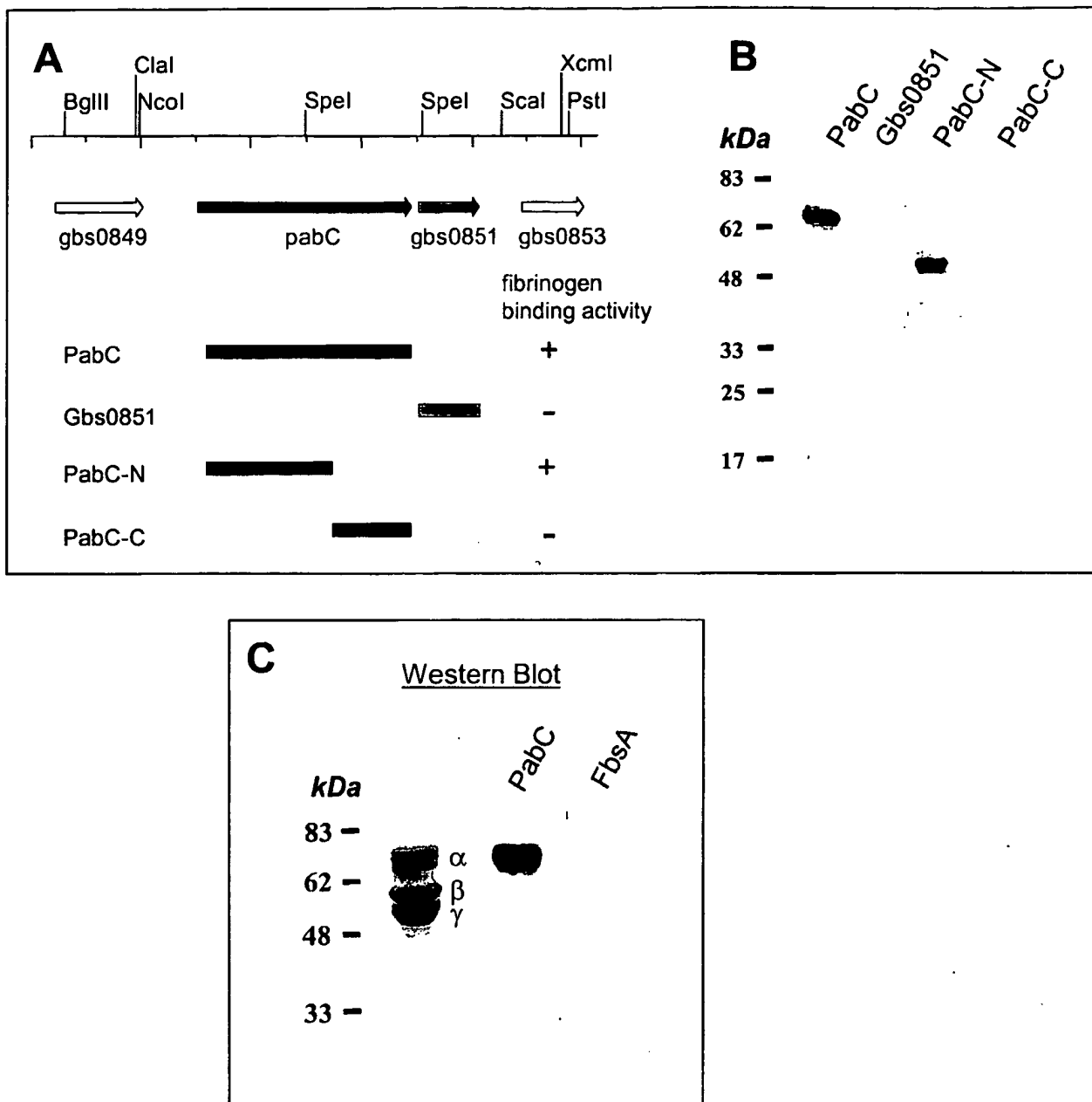


Fig. 31

Inventor: Reinscheid et al.

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Docket No.: 116676-006

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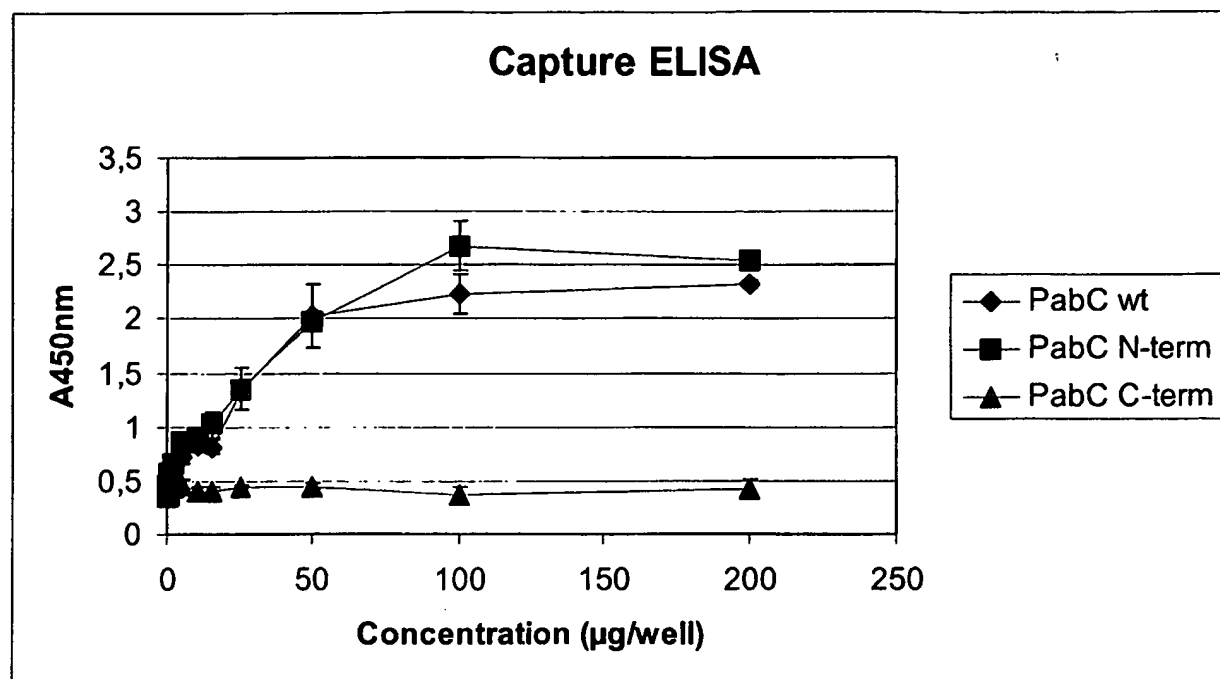


Fig. 32

Inventor: Reinscheid et al.

App. No.: Unknown

Docket No.: 116676-006

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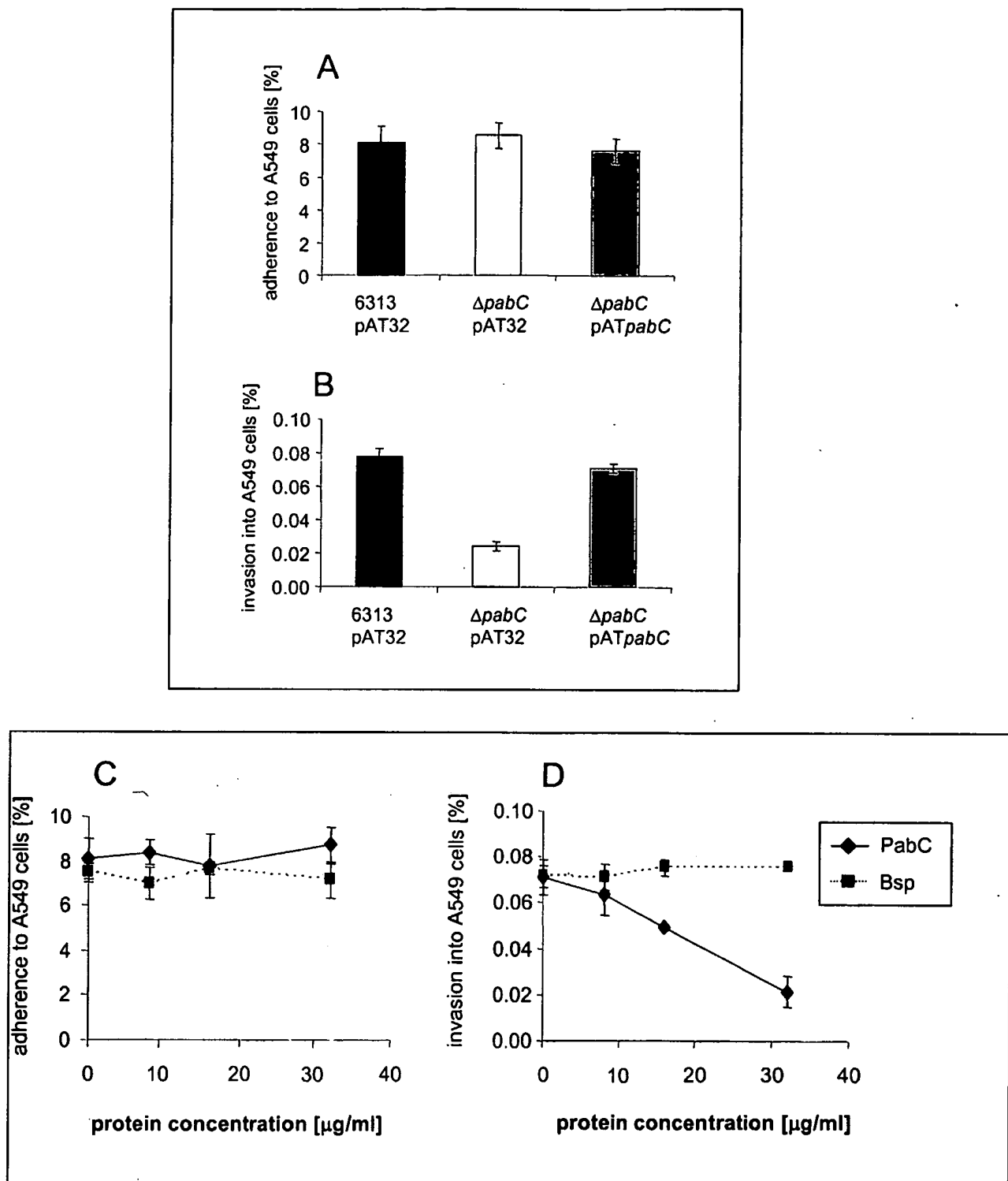


Fig. 33

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